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OM nucleic - nucleic search, using sw model

Run on: May 10, 2005, 16:50:43 ; Search time 279.152 Seconds
(without alignments)
9724.375 Million cell updates/sec

Title: US-10-044-205A-3

Perfect score: 1659

Sequence: 1 atggtgacatgggggccc.....ctggcgtgtttgtattg 1659

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA.*

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*

5: /cgn2_6/ptodata/1/ina/PTCUS_COMB.seq.*

6: /cgn2_6/ptodata/1/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1655.8	99.8	2249	US-09-802-117-5	Sequence 5, Appli
2	1655.8	99.8	2249	US-10-217-745-5	Sequence 5, Appli
3	1655.4	99.8	1662	US-09-802-117-1	Sequence 1, Appli
4	1655.4	99.8	1662	US-10-217-745-1	Sequence 1, Appli
5	1654.2	99.7	1662	US-09-738-894A-1	Sequence 1, Appli
6	1654.2	99.7	1662	US-09-964-469-1	Sequence 1, Appli
7	1046.8	63.1	1062	US-09-802-117-3	Sequence 3, Appli
8	1046.8	63.1	1062	US-10-217-745-3	Sequence 3, Appli
9	617.4	37.2	36651	US-09-738-894A-3	Sequence 3, Appli
10	617.4	37.2	36651	US-09-964-469-3	Sequence 3, Appli
11	419.8	25.3	2848	US-08-464-954A-2	Sequence 2, Appli
12	418.2	25.2	2204	US-08-221-817-12	Sequence 12, Appli
13	418.2	25.2	2204	US-08-454-439-12	Sequence 12, Appli
14	418.2	25.2	2204	PCT-US94-10487-12	Sequence 12, Appli
15	395.8	23.9	1983	US-08-221-817-21	Sequence 21, Appli
16	395.8	23.9	1983	US-08-454-439-21	Sequence 21, Appli
17	395.8	23.9	1983	PCT-US94-10487-21	Sequence 21, Appli
18	389.4	23.5	2206	US-08-221-817-10	Sequence 10, Appli
19	389.4	23.5	2206	US-08-454-439-10	Sequence 10, Appli
20	389.4	23.5	2206	PCT-US94-10487-10	Sequence 10, Appli
21	373	22.5	2511	US-09-417-197-60	Sequence 60, Appli
22	373	22.5	2529	US-09-417-197-40	Sequence 42, Appli
23	373	22.5	2557	US-09-016-434-1298	Sequence 1298, Ap
24	366.6	22.1	2557	US-08-464-954A-1	Sequence 1, Appli
25	320.6	19.3	2017	US-09-614-748A-8	Sequence 8, Appli
26	320.6	19.3	2113	US-09-614-748A-7	Sequence 7, Appli
27	311.6	18.8	1879	US-09-614-748A-10	Sequence 10, Appli

28 311.6 18.8 1886 1 US-07-980-526-1 Sequence 1, Appli

29 311.6 18.8 1975 4 US-09-614-748A-9 Sequence 9, Appli

30 253.2 15.3 1305 4 US-09-614-748A-12 Sequence 12, Appli

31 251.6 15.2 1420 4 US-09-614-748A-11 Sequence 11, Appli

32 151 9.1 3422 4 US-09-949-016-1312 Sequence 1312, Ap

33 130.8 7.9 2067 4 US-09-016-434-1306 Sequence 1306, Ap

34 129.2 7.8 3628 4 US-09-949-016-4773 Sequence 4773, Ap

35 127.6 7.7 2362 4 US-09-620-312D-273 Sequence 273, App

36 116.4 7.0 294 1 US-08-221-817-9 Sequence 9, Appli

37 116.4 7.0 294 1 US-08-454-439-9 Sequence 9, Appli

38 116.4 7.0 294 5 PCT-US94-10487-9 Patent No. 5266464

39 112.8 6.8 2599 6 5266464-1 Patent No. 5266464

40 112.8 6.8 2599 6 5266464-1 Patent No. 5266464

41 112 6.8 1788 4 US-09-417-197-68 Sequence 68, Appli

42 110.8 6.7 1191 4 US-09-841-683-10 Sequence 10, Appli

43 110.8 6.7 1224 4 US-09-841-683-8 Sequence 8, Appli

44 110.8 6.7 1485 4 US-09-801-876B-1 Sequence 1, Appli

45 110.8 6.7 1485 4 US-10-254-869-1 Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-802-117-5
; Sequence 5, Application US/09802117
; Patent No. 644456
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; TITLE OF INVENTION: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 644456el Human G-Coupled Protein Receptor Kinases and Polynu
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/09/802.117
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/188,449
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2249
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-802-117-5

Query Match 99.8%; Score 1655.8; DB 3; Length 2249;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1657; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGCTGGACATGGGGGCCCTGGACAACTGATCGCAACACCGCTACTCGAGGCGCGG 60
Db 354 ATGCTGGACATGGGGGCCCTGGACAACTGATCGCAACACCGCTACTCGAGGCGCGG 413

Qy 61 AAGCCCTCGGACTCGACAGCAAGAGCTGAGCGGGCGGCGGTAGCTGGCCCTGCCC 120
Db 414 AAGCCCTCGGACTCGACAGCAAGAGCTGAGCGGGCGGCGGTAGCTGGCCCTGCCC 473

Qy 121 GGGCTGAGGGCTGGGGGAGCTCGGCAAGAGCTGCTCCCTGAACTTCCACAGGCTGTGT 180
Db 474 GGGCTGAGGGCTGGGGGAGCTCGGCAAGAGCTGCTCCCTGAACTTCCACAGGCTGTGT 533

Qy 181 GAGCAGCAGCCCATCGGTGCGCGGCTCTTCCGTGACTTCTAGCCACAGTGCACAGTTC 240
Db 534 GAGCAGCAGCCCATCGGTGCGCGGCTCTTCCGTGACTTCTAGCCACAGTGCACAGTTC 593

Qy 241 CGCAAGCGCGCAACTTCTTAGAGAGAGCTGGAGAACTGGGAGCTGGCGAGGAGGCC 300
Db 594 CGCAAGCGCGCAACTTCTTAGAGAGAGCTGGAGAACTGGGAGCTGGCGAGGAGGCC 653

Qy 301 ACCAAAGACAGCGGCTGCGAGGGGCTGGTGCCACTTGTGGAGTGGCCCTGCCCGGG 360
Db 654 ACCAAAGACAGCGGCTGCGAGGGGCTGGTGCCACTTGTGGAGTGGCCCTGCCCGGG 713

QY	1441	AAAGACATCGCTGAAATTTGATGATTTCTCTGAGGTTTCGGGGGTGGAATTTTATGACAAA	1500
Db	1794	AAAGACATCGCTGAAATTTGATGATTTCTCTGAGGTTTCGGGGGTGGAATTTTATGACAAA	1853
QY	1501	GATAAGCAGTCTCTCAAAAACCTTTGCGACAGGTCTGCTTCTATAGCATGGCAGGAAGA	1560
Db	1854	GATAAGCAGTCTCTCAAAAACCTTTGCGACAGGTCTGCTTCTATAGCATGGCAGGAAGA	1913
QY	1561	ATTATAGAAACGGGACTGTTTTCAGGAACCTGATGATGACCCCAACAGACCTACGGGTTGTGAG	1620
Db	1914	ATTATAGAAACGGGACTGTTTTCAGGAACCTGATGATGACCCCAACAGACCTACGGGTTGTGAG	1973
QY	1621	GAGGGTAATTCATCCAAAGTCTGGCGTGTGTTTGTATTG	1659
Db	1974	GAGGGTAATTCATCCAAAGTCTGGCGTGTGTTTGTATTG	2012
RESULT 2			
US-10-217-745-5			
; Sequence 5, Application US/10217745			
; Patent No. 6838275			
; GENERAL INFORMATION:			
; APPLICANT: Walke, D. Wade			
; APPLICANT: Wilganowski, Nathaniel L.			
; APPLICANT: Turner, C. Alexander Jr.			
; TITLE OF INVENTION: No. 6838275el Human G-Coupled Protein Receptor Kinases and			
; TITLE OF INVENTION: Polynucleotides			
; TITLE OF INVENTION: Encoding the Same			
; FILE REFERENCE: LEX-0147-USA			
; CURRENT APPLICATION NUMBER: US/10/217,745			
; CURRENT FILING DATE: 2002-08-12			
; PRIOR APPLICATION NUMBER: US/09/802,117			
; PRIOR FILING DATE: 2001-03-08			
; NUMBER OF SEQ ID NOS: 5			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 5			
; LENGTH: 2249			
; TYPE: DNA			
; ORGANISM: homo sapiens			
US-10-217-745-5			
Query Match 99.8%; Score 1655.8; DB 4; Length 2249;			
Best Local Similarity 99.9%; Pred. No. 0;			
Matches 1657; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
QY	1	ATGTTGACATGTTGGGGCCCTGGACAACTGATCGCCAAACCGCTACCTGACGCGCCGG	60
Db	354	ATGTTGACATGTTGGGGCCCTGGACAACTGATCGCCAAACCGCTACCTGACGCGCCGG	413
QY	61	AAGCCCTCGGACTGCGACAGCAAGAGCTGCGCGGGCGGCGGTAGCTGGCCCTGCCC	120
Db	414	AAGCCCTCGGACTGCGACAGCAAGAGCTGCGCGGGCGGCGGTAGCTGGCCCTGCCC	473
QY	121	GGGCTGACAGGCTGCGCGGAGCTCGCCAGAAAGTGTCCCTGAACTTCCACAGCTGTGT	180
Db	474	GGGCTGACAGGCTGCGCGGAGCTCGCCAGAAAGTGTCCCTGAACTTCCACAGCTGTGT	533
QY	181	GAGCGAGAGCCCATCGGTCGCGCCCTCTTCGCTGACTTCTTAGCCACAGTGCACAGTTC	240
Db	534	GAGCGAGAGCCCATCGGTCGCGCCCTCTTCGCTGACTTCTTAGCCACAGTGCACAGTTC	593
QY	241	CGCAAGGGGGCAACCTTCTTAGAGGACGTCGAGAACTGGGAGCTGGCGAGGAGGACCC	300
Db	594	CGCAAGGGGGCAACCTTCTTAGAGGACGTCGAGAACTGGGAGCTGGCGAGGAGGACCC	653
QY	301	ACCAAGACAGCGGCTGCGAGGGGTGGCCACTTGTGCGAGTGCCTTCCCGCGGG	360
Db	654	ACCAAGACAGCGGCTGCGAGGGGTGGCCACTTGTGCGAGTGCCTTCCCGCGGG	713
QY	361	AAACCGCAACCTTCTCTAGCGAGCGGCTGGCCACCAAGTGCAGGAGCCACCTAG	420
Db	714	AAACCGCAACCTTCTCTAGCGAGCGGCTGGCCACCAAGTGCAGGAGCCACCTAG	773

QY 421 GAAGAGCGAGTGGCTGACGCTGCCGCAAGGCTGAGGCCATGGCTTTCTTGCAGAG 480
DB 774 GAAGAGCGAGTGGCTGACGCTGCCGCAAGGCTGAGGCCATGGCTTTCTTGCAGAG 833
QY 481 CAGCCCTTTAAGGATTTCTGACGAGCGCTTCTACGACAAAGTTTCTGCAAGTGAACATC 540
DB 834 CAGCCCTTTAAGGATTTCTGACGAGCGCTTCTACGACAAAGTTTCTGCAAGTGAACATC 893
QY 541 TTCGAGATGCAACCGAGTGTGACAAAGTACTTCACTGAGTTCAGAGTGTGCGGGAAGGT 600
DB 894 TTCGAGATGCAACCGAGTGTGACAAAGTACTTCACTGAGTTCAGAGTGTGCGGGAAGGT 953
QY 601 GCTTTTGGGAGGTATGTCCTCCAGGTGAAACACATGCGGAAAGTATGCTGCTGTAAG 660
DB 954 GCTTTTGGGAGGTATGTCCTCCAGGTGAAACACATGCGGAAAGTATGCTGCTGTAAG 1013
QY 661 AACTCGGACAAAGCGGCTGAAGAAAGGTGGCGAAGATGGCTCTCTTGGAAAG 720
DB 1014 AACTCGGACAAAGCGGCTGAAGAAAGGTGGCGAAGATGGCTCTCTTGGAAAG 1073
QY 721 GAAATCTTGGAGAGGTGACGAGCCCTTTCATGTCTCTCTGCGCTATGCTTGGAGGC 780
DB 1074 GAAATCTTGGAGAGGTGACGAGCCCTTTCATGTCTCTCTGCGCTATGCTTGGAGGC 1133
QY 781 AAGACCCATCTCTGCTTGTCTATGAGCCTGATGAATGGGGAGACCTCAAGTTCACATC 840
DB 1134 AAGACCCATCTCTGCTTGTCTATGAGCCTGATGAATGGGGAGACCTCAAGTTCACATC 1193
QY 841 TACAACGTGGGACGCGTGGCTGGACATGACCGGCTGATCTTTTACTCGGCCAGATA 900
DB 1194 TACAACGTGGGACGCGTGGCTGGACATGACCGGCTGATCTTTTACTCGGCCAGATA 1253
QY 901 GCCTGTGGGATCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCTGAG 960
DB 1254 GCCTGTGGGATCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCTGAG 1313
QY 961 AATGTCTTCTGATGACCTCGGAACTGACGCTTATGACCTGGGGTGGCGGTGAG 1020
DB 1314 AATGTCTTCTGATGACCTCGGAACTGACGCTTATGACCTGGGGTGGCGGTGAG 1373
QY 1021 ATGAAGGTGGCAAGCCATACCCAGAGGCTGGAACCAATGTTTACATGCTCCTGAG 1080
DB 1374 ATGAAGGTGGCAAGCCATACCCAGAGGCTGGAACCAATGTTTACATGCTCCTGAG 1433
QY 1081 ATCTAATGGAAGGTAAAGTTATTTCTATCTCTGGAAGTGGTGGCATGGGATGACGC 1140
DB 1434 ATCTAATGGAAGGTAAAGTTATTTCTATCTCTGGAAGTGGTGGCATGGGATGACGC 1493
QY 1141 ATTTATGAAATGGTGTGCGAGCAACACCATTTCAAAGATTACAAGAAAGGTCAATAA 1200
DB 1494 ATTTATGAAATGGTGTGCGAGCAACACCATTTCAAAGATTACAAGAAAGGTCAATAA 1553
QY 1201 GAGGATCTGAAGCAAGAACTCTGCAAGCGAGGTCAAATTCACAGCATGAATTTACA 1260
DB 1554 GAGGATCTGAAGCAAGAACTCTGCAAGCGAGGTCAAATTCACAGCATGAATTTACA 1613
QY 1261 GAGGAAGCAAAAGATATTTGCAAGGCTCTTCTTGGCTTAAGAAACCAAGCAAGCTTAGGA 1320
DB 1614 GAGGAAGCAAAAGATATTTGCAAGGCTCTTCTTGGCTTAAGAAACCAAGCAAGCTTAGGA 1673
QY 1321 AGCAGAGAAAGTCTGATGATCCCAAGGAAACATCATTTCTTTAAACGATCAACTTTCT 1380
DB 1674 AGCAGAGAAAGTCTGATGATCCCAAGGAAACATCATTTCTTTAAACGATCAACTTTCT 1733
QY 1381 CGCTTGGAGCTGGCTAATTAACCCCATTTGTCAGACCCCTTCAAGTGGTTATGCC 1440
DB 1734 CGCTTGGAGCTGGCTAATTAACCCCATTTGTCAGACCCCTTCAAGTGGTTATGCC 1793
QY 1441 AAGACATCGCTGAAATGATTTCTTCTGAGGTTTCGGGGGTGGAATTTGATGACAAA 1500
DB 1794 AAGACATCGCTGAAATGATTTCTTCTGAGGTTTCGGGGGTGGAATTTGATGACAAA 1853
QY 1501 GATAAGCAGTTCTTCAAAACATTTTGCAGACGCTGCTGTTCTTATAGCATGGCAGGA 1560

DB 1854 GATAAGCAGTTCTTCAAAACATTTTCGACAGGTGCTGTTCTTATAGCATGGCAGGA 1913
QY 1561 ATTATAGAAACGGGACTGTTTGGAGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
DB 1914 ATTATAGAAACGGGACTGTTTGGAGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1973
QY 1621 GAGGTAATATCATCAAGTCTGGCGTGTGTTTGTATTG 1659
DB 1974 GAGGTAATATCATCAAGTCTGGCGTGTGTTTGTATTG 2012

RESULT 3
US-09-802-117-1
; Sequence 1, Application US/09802117
; Patent No. 644456
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; TITLE OF INVENTION: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 644456el Human G-Coupled Protein Receptor Kinases and Polyn
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/09/802,117
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/188,449
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-802-117-1

Query Match 99.8%; Score 1655.4; DB 3; Length 1662;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1656; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGTGGACATGGGGGCCCTGGACAACTGATCGCAACACCGCTACTCTGACAGCCCGG 60
DB 1 ATGGTGGACATGGGGGCCCTGGAYAACCTGATCGCAACACCGCTACTCTGACAGCCCGG 60
QY 61 AAGCCCTCGGACTGCGACAGCAAAAGAGCTGAGCGCGCGGCTAGCCTTGCCCTGCCC 120
DB 61 AAGCCCTCGGACTGCGACAGCAAAAGAGCTGAGCGCGCGGCTAGCCTTGCCCTGCCC 120
QY 121 GGGCTGACAGGCTGGCGGAGCTCGCCAGAAAGCTGCTCCCTGAACCTTCCACAGCCTGTGT 180
DB 121 GGGCTGACAGGCTGGCGGAGCTCGCCAGAAAGCTGCTCCCTGAACCTTCCACAGCCTGTGT 180
QY 181 GAGCAGCAGCCATCGGTGCGCGCTCTTTCGTGACTTCTTAGCCACAGTGCACAGTTTC 240
DB 181 GAGCAGCAGCCATCGGTGCGCGCTCTTTCGTGACTTCTTAGCCACAGTGCACAGTTTC 240
QY 241 CGCAAGCGGCAACCTCTCTAGAGAGCTGCGAGAACTGGGAGCTGGCGAGGAGGACCC 300
DB 241 CGCAAGCGGCAACCTCTCTAGAGAGCTGCGAGAACTGGGAGCTGGCGAGGAGGACCC 300
QY 301 ACCAAAGACAGCGGCTGACAGGGGTGTGGCCACTTGTGCGAGTGCCTTCCCGCGGG 360
DB 301 ACCAAAGACAGCGGCTGACAGGGGTGTGGCCACTTGTGCGAGTGCCTTCCCGCGGG 360
QY 361 AACCGCAACCTTCTTCAGCAGCGCTGGCCCAAGTGCAGAGCAGCCACCACTGAG 420
DB 361 AACCGCAACCTTCTTCAGCAGCGCTGGCCCAAGTGCAGAGCAGCCACCACTGAG 420
QY 421 GAAGAGCAGTGGCTGACAGTGAAGCTGAGGCGCATGGCTTTCTTGAAGAG 480
DB 421 GAAGAGCAGTGGCTGACAGTGAAGCTGAGGCGCATGGCTTTCTTGAAGAG 480
QY 481 CAGCCCTTTAAGGATTTGCTGACAGCGCCTTTCTACGACAAAGTTTCTGACGTGGAACATC 540

Db 481 CAGCCCTTAAGGATTTCTGTCAGCAGCGCTTCTACGACAAAGTTTCTGCGAGTGAAACTC 540
Qy 541 TTCGAGATGCAACCAAGTCTCAGCAAGTACTTCTACTGAGTTCAGAGTCTCGGGAAAGGT 600
Db 541 TTCGAGATGCAACCAAGTCTCAGCAAGTACTTCTACTGAGTTCAGAGTCTCGGGAAAGGT 600
Qy 601 GGTTTTGGGAGGTATGTCGCTGACGCTGAGGCTGAAACACTGCGGAAAGATGATGCTGTAAAG 660
Db 601 GGTTTTGGGAGGTATGTCGCTGACGCTGAGGCTGAAACACTGCGGAAAGATGATGCTGTAAAG 660
Qy 661 AAATGGGACAAAGACGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
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Qy 721 GAAATCTTGGGAGAGGTGAGAGGCTTTCATGTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db 721 GAAATCTTGGGAGAGGTGAGAGGCTTTCATGTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Qy 781 AAGACCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
Db 781 AAGACCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
Qy 841 TACAACTGGGACGCGTGGCTGGACATGAGCGGGTGATCTTTTACTCGGCGCCAGATA 900
Db 841 TACAACTGGGACGCGTGGCTGGACATGAGCGGGTGATCTTTTACTCGGCGCCAGATA 900
Qy 901 GCCTGTGGATGCTGCACTCATGAACCTGCGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Db 901 GCCTGTGGATGCTGCACTCATGAACCTGCGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Qy 961 AATGTGCTTCTGATGATCTGCGCAACTGCGGATGATCTGACCTGGGCTGGCGCTGGAG 1020
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Qy 1021 ATGAAGGTTGGAAGCCCATACCCAGAGGGTGGAAACAAATGGTTAATAGGCTCCTGAG 1080
Db 1021 ATGAAGGTTGGAAGCCCATACCCAGAGGGTGGAAACAAATGGTTAATAGGCTCCTGAG 1080
Qy 1081 ATCTTAATGGAAGGTAAGTTATTCCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
Db 1081 ATCTTAATGGAAGGTAAGTTATTCCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
Qy 1141 ATTTATGAAATGGTTGCTGGAAGCAACCAATTCAGAGATTACAAGGAAAGGTCAGTAAA 1200
Db 1141 ATTTATGAAATGGTTGCTGGAAGCAACCAATTCAGAGATTACAAGGAAAGGTCAGTAAA 1200
Qy 1201 GAGGATCTGAAGCAAGAACTCTGCAAGACGAGGTCAAAATTCAGGATGATTAACCTTACA 1260
Db 1201 GAGGATCTGAAGCAAGAACTCTGCAAGACGAGGTCAAAATTCAGGATGATTAACCTTACA 1260
Qy 1261 GAGGAGCAAAAGATATTTGAGGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
Db 1261 GAGGAGCAAAAGATATTTGAGGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
Qy 1321 AGCAGAGAAAGTCTGATGATCCAGGAAACATCAATTTCTTTAAACGATCAACTTTCT 1380
Db 1321 AGCAGAGAAAGTCTGATGATCCAGGAAACATCAATTTCTTTAAACGATCAACTTTCT 1380
Qy 1381 CGCTGGAAGTGGCTTAATGAAACCCCATTTTGGCCAGACCCCTTCACTGCTGCTTATGCC 1440
Db 1381 CGCTGGAAGTGGCTTAATGAAACCCCATTTTGGCCAGACCCCTTCACTGCTGCTTATGCC 1440
Qy 1441 AAGACATCGCTGAAATGATGATTTCTGAGTTTCGGGGTGGAAATTCATGACAAA 1500
Db 1441 AAGACATCGCTGAAATGATGATTTCTGAGTTTCGGGGTGGAAATTCATGACAAA 1500
Qy 1501 GATAAGCAGTCTTCAAAAATTTTGGCAGAGGTGCTGTTTCTTATAGCATGGCAGGAGAA 1560
Db 1501 GATAAGCAGTCTTCAAAAATTTTGGCAGAGGTGCTGTTTCTTATAGCATGGCAGGAGAA 1560
Qy 1561 ATTATAGAACGGGACTTTTGGAGAACTGAAATGACCCCAACAGACTACGGGTGTGAG 1620
Db 1561 ATTATAGAACGGGACTTTTGGAGAACTGAAATGACCCCAACAGACTACGGGTGTGAG 1620

Qy 1621 GAGGTAATTCATCCAGTCTGGGCTGTGTTGTTGTTATTTG 1659
Db 1621 GAGGTAATTCATCCAGTCTGGGCTGTGTTGTTGTTATTTG 1659

RESULT 4

US-10-217-745-1
; Sequence 1, Application US/10217745
; Patent No. 6838275
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6838275el Human G-Coupled Protein Receptor Kinases and
; TITLE OF INVENTION: Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/10/217,745
; PRIOR FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US/09/802,117
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-217-745-1.

Query Match 99.8%; Score 1655.4; DB 4; Length 1662;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1656; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGTGTGACATGGGGCCCTGGACAACTGATCCCAACACCGCTACTCTCAGGCCCGG 60
Db 1 ATGTGTGACATGGGGCCCTGGAACTGATCCCAACACCGCTACTCTCAGGCCCGG 60
Qy 61 AAGCCCTCGGACTCGGAGCAAGAGAGCTGAGCGGGGGGGGGCTAGCTGGCCCTGCCC 120
Db 61 AAGCCCTCGGACTCGGAGCAAGAGAGCTGAGCGGGGGGGGGCTAGCTGGCCCTGCCC 120
Qy 121 GGGCTGCAAGGCTCGGGGAGCTCGCCAGAAAGCTGCTCCCTGAACTTCCAGAGCTGTGT 180
Db 121 GGGCTGCAAGGCTCGGGGAGCTCGCCAGAAAGCTGCTCCCTGAACTTCCAGAGCTGTGT 180
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Db 181 GAGCAGAGCCCATCTCGGCTCGCGCTCTTCCGTGACTTCTTAGCCACAGTCCCAAGTTC 240
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Qy 301 ACCAAGAAGCAGCGGCTCGAGGGCTGCTGGCCACTTGTGCGAGTGGCCCTGCCCCGGGG 360
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Qy 481 CAGCCCTTTAAGGATTTCTGACAGAGCGCTTCTACGACAAAGTTTCTGAGTGGAAACTC 540
Db 481 CAGCCCTTTAAGGATTTCTGACAGAGCGCTTCTACGACAAAGTTTCTGAGTGGAAACTC 540
Qy 541 TTCGAGATGCAACCAAGTCTCAGCAAGTACTTCACTGAGTTCAGAGTGTCTGGGAAAGGT 600
Db 541 TTCGAGATGCAACCAAGTCTCAGCAAGTACTTCACTGAGTTCAGAGTGTCTGGGAAAGGT 600


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QY 601 GGTGTTGGGAGGTATGTGCGCTCAGGTGAACAACTGGGAAGATGTATGCTGTAAAG 660
Db 601 GGTGTTGGGAGGTATGTGCGCTCAGGTGAACAACTGGGAAGATGTATGCTGTAAAG 660
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Db 661 AAATCTGGACAAGACGGCTGAAGAAAGAGTGGCGAAGATGGCTCTCTTTGGAAAG 720
QY 721 GAAATCTTGGAGAAGTCAAGAGCCCTTTTCATTTGTTCTCTCGCCCTATGCTTTCAGAGC 780
Db 721 GAAATCTTGGAGAAGTCAAGAGCCCTTTTCATTTGTTCTCTCGCCCTATGCTTTCAGAGC 780
QY 781 AAGACCCATCTCTGCTTGTATGAGCCTGTGAATGGGGAGACCTCAAGTTCCACATC 840
Db 781 AAGACCCATCTCTGCTTGTATGAGCCTGTGAATGGGGAGACCTCAAGTTCCACATC 840
QY 841 TACAACGTGGGACCGCTGGCTGACATGACGCGGGTGATCTTTTACTCGGCCAGATA 900
Db 841 TACAACGTGGGACCGCTGGCTGACATGACGCGGGTGATCTTTTACTCGGCCAGATA 900
QY 901 GCCTGTGGATGCTGCACCTCCATGAACCTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960
Db 901 GCCTGTGGATGCTGCACCTCCATGAACCTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960
QY 961 AATGTCTTCTGGATGACCTCGGCAACTGCGAGGTTATCTGACCTGGGGTGGCCGTGGAG 1020
Db 961 AATGTCTTCTGGATGACCTCGGCAACTGCGAGGTTATCTGACCTGGGGTGGCCGTGGAG 1020
QY 1021 ATGAGGGTGGCAAGCCCATCACAGAGGGCTGCAACCAATGGTTACATGGCTCCTGAG 1080
Db 1021 ATGAGGGTGGCAAGCCCATCACAGAGGGCTGCAACCAATGGTTACATGGCTCCTGAG 1080
QY 1081 ATCTTAATGGAAGAGTAAATTTCTTATCTGTGGACTGTTTGGCCATGGATGCGAGC 1140
Db 1081 ATCTTAATGGAAGAGTAAATTTCTTATCTGTGGACTGTTTGGCCATGGATGCGAGC 1140
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Db 1141 ATTTATGAAATGTTGCTGGACGAAACACCAATTCAGAGATTAACAAGAAAGGTCAATAA 1200
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Db 1201 GAGGATCTGAAGCAAGAACTCTGCAGAGAGGTCAAAATTCAGCATGATTAACCTTACA 1260
QY 1261 GAGGAAGCAAGAAATATTTGCAAGGCTCTTCTTGGCTTAAGAAACCAAGACGCTTAGGA 1320
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QY 1321 AGCAGAGAAAGTCTGATGATCCAGGAAACATCAATTTCTTTAAACGATCAACTTCTCT 1380
Db 1321 AGCAGAGAAAGTCTGATGATCCAGGAAACATCAATTTCTTTAAACGATCAACTTCTCT 1380
QY 1381 CCGCTGGAAGCTGGCTTAATGAAACCCCATTTGTGCGAGACCCCTTCACTGTTTATGCC 1440
Db 1381 CCGCTGGAAGCTGGCTTAATGAAACCCCATTTGTGCGAGACCCCTTCACTGTTTATGCC 1440
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Db 1441 AAGACATGCTGAAATGATCATTTCTGAGGTTGGGGGTGGAAATTTGATGACAAA 1500
QY 1501 GATAAGCAGTTCTTCAAAAATTTTGGACAGAGTGTGTTCTTATAGCATGGCAGGAAGAA 1560
Db 1501 GATAAGCAGTTCTTCAAAAATTTTGGACAGAGTGTGTTCTTATAGCATGGCAGGAAGAA 1560
QY 1561 ATTATAGAAACGGGACTGTTTGAAGAACTGAATGACCCCAACAGACCTACCGGTTGTGAG 1620
Db 1561 ATTATAGAAACGGGACTGTTTGAAGAACTGAATGACCCCAACAGACCTACCGGTTGTGAG 1620
QY 1621 GAGGGTAATTCATCCAGTCTGGCGTGTGTTTGTATTG 1659
Db 1621 GAGGGTAATTCATCCAGTCTGGCGTGTGTTTGTATTG 1659
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RESULT 5
US-09-738-894A-1
; Sequence 1, Application US/09738894A
; Patent No. 6331423
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CLO00636
; CURRENT APPLICATION NUMBER: US/09/738,894A
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Human
US-09-738-894A-1
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Query Match 99.7%; Score 1654.2; DB 3; Length 1662;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1656; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 1 ATGTTGGAATGTTGGGGCCCTCGAACCTGATCGCCAAACACCGCTTACTGTGAGGCCCGG 60
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Db 61 AAGCCCTCGGACTGCGACAGCAAGAGCTGCGAGCGCGGCGGTAGCTGSCCTGCCCC 120
QY 121 GGGCTGCAAGGCTGCGCGGAGCTCCGCCAGAAAGCTGTCCCTGAACTTCCACAGCTGTGT 180
Db 121 GGGCTGCAAGGCTGCGCGGAGCTCCGCCAGAAAGCTGTCCCTGAACTTCCACAGCTGTGT 180
QY 181 GAGCAGCAGCCCATCGTTCGCGGCTCTTCCTGAGTCTTCTAGCCACAGTGCCTGTTTC 240
Db 181 GAGCAGCAGCCCATCGTTCGCGGCTCTTCCTGAGTCTTCTAGCCACAGTGCCTGTTTC 240
QY 241 CGCAAGCGGCAACCTTCTTAGAGCACTGGAGCTGGGAGCTGGCGAGGAGGACCC 300
Db 241 CGCAAGCGGCAACCTTCTTAGAGCACTGGAGCTGGGAGCTGGCGAGGAGGACCC 300
QY 301 ACCAAGACAGCGGCTGCGAGGCTGTGGCCACTTGTGCGAGTGCCTGCCCGGG 360
Db 301 ACCAAGACAGCGGCTGCGAGGCTGTGGCCACTTGTGCGAGTGCCTGCCCGGG 360
QY 361 AACCCGCAACCTTCTCAGCCAGCCCGTGGCCACCAAGTGCACAGCACCACCTGAG 420
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QY 421 GAAGAGCAGTGGCTGAGTGCAGCTGCGCAAGGCTGAGGCCATGGCTTCTTTCAGAG 480
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Db 661 AAATCTGGACAAGACGGCTGAAGAAAGAGTGGCGAAGATGGCTCTCTTTGGAAAG 720
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Db 781 AAGACCCATCTCTGCTTGTATGAGCTGATGATGGGGAGAGCTCAAGTTCCACATC 840
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Db 841 TACAACTGGGACGCGTGGCTGACATGACAGCCGGTGAATCTTCTGCGCCAGATA 900
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Db 1381 CCGCTGGAAGCTGGCTAATTTGAACCCCATTTGCGCAGACCTTCAAGTGGTTATGCC 1440
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Db 1501 GATAAGCAGTTCTTCAAAACCTTTCGACAGTGTCTGTTCTATAGCATGGCAGAGAA 1560
QY 1561 ATTATAGAAAAGGAGTGTGTTGAGGAATGATGATGATGATGATGATGATGATGATGAT 1620
Db 1561 ATTATAGAAAAGGAGTGTGTTGAGGAATGATGATGATGATGATGATGATGATGATGAT 1620
QY 1621 GAGGTAATTCATCAAGTCTGGCGTGTGTTGTTATTG 1659
Db 1621 GAGGTAATTCATCAAGTCTGGCGTGTGTTGTTATTG 1659
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RESULT 6

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US-09-964-469-1
; Sequence 1, Application US/09964469
; Patent No. 6579709
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
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; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO00636DIV
; CURRENT APPLICATION NUMBER: US/09/964,469
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 60/208,331
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: 09/738,894
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Human
US-09-964-469-1
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Query Match 99.7%; Score 1654.2; DB 4; Length 1662;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1656; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ATGTGTGACATGGGGGCGCTCGACAACTGATCGCAACACCGCTACTCTGAGGCCGG 60
Db 1 ATGTGTGACATGGGGGCGCTCGACAACTGATCGCAACACCGCTACTCTGAGGCCGG 60
QY 61 AAGCCCTCGACTGCGACAGCAAAAGAGCTGAGCGGGGGGGGGCTAGCCTGGCCCTGCC 120
Db 61 AAGCCCTCGACTGCGACAGCAAAAGAGCTGAGCGGGGGGGGGCTAGCCTGGCCCTGCC 120
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Db 121 GGGCTGACGGGCTCGGGGAGCTCGCAGAGAGCTGCTCCCTGAACTTCCACAGACCTGT 180
QY 181 GAGCAGCAGCCCATCGGTGCGCGCTCTTCCGTGACTTCTTAGCCACAGTGCACAGTTC 240
Db 181 GAGCAGCAGCCCATCGGTGCGCGCTCTTCCGTGACTTCTTAGCCACAGTGCACAGTTC 240
QY 241 CGCAAGGCGGCAACCTTCTTAGAGAGAGCTGCGAGAACTGGGAGCTGGCGGAGGAGGCC 300
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QY 301 ACCAAGACAGCGCGCTGCGGGGCTGGTGGCCACTTGTGAGTGGCCCTGCCCCGGGG 360
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QY 361 AACCCTGCAACCTTCTCAGCAGCGCGCTGCGCCACCAAGTGCACAGCAGCCACCTGAG 420
Db 361 AACCCTGCAACCTTCTCAGCAGCGCGCTGCGCCACCAAGTGCACAGCAGCCACCTGAG 420
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Db 721 GAAATCTTGGAGAGGCTGAGGTAAGAAAGAGTGGCGGAGAGATGGCTCTCTTGGAAAG 780
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1621 GAGGTAATTCATCAAGCTGGCGGTGTTGTTTATTG 1659

RESULT 7
US-09-802-117-3
; Sequence 3, Application US/09802117
; Patent No. 644456
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 644456el Human G-Coupled Protein Receptor Kinases and Polynu
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/09/802,117
; CURRENT FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: US 60/188,449
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-802-117-3

Query Match 63.1%; Score 1046.8; DB 3; Length 1062;
Best Local Similarity 99.8%; Pred. No. 5.8e-259; Indels 0; Gaps 0;
Matches 1048; Conservative 0; Mismatches 2;

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DB 61 AAGCCCTCGGATGCGACAGCAAGAGCTGACGCGCGCGCGCTAGCTGCGCTTGCCTC 120
QY 121 GGGCTGCAAGGCTGCGCGAGCTCGCCAGAGCTGCTGAACTTCCACAGCTGTGT 180
DB 121 GGGCTGCAAGGCTGCGCGAGCTCGCCAGAGCTGCTGAACTTCCACAGCTGTGT 180
QY 181 GAGCAGACGCCATCGGTGCGCGCTCTTCCGTGACTTCTAGCCACAGTGCCTCAGTTC 240
DB 181 GAGCAGACGCCATCGGTGCGCGCTCTTCCGTGACTTCTAGCCACAGTGCCTCAGTTC 240
QY 241 CGCAAGCGCGCAACCTTCTAGAGGACGTGCGAGAACTGGGAGCTGGCGAGGAGGCC 300
DB 241 CGCAAGCGCGCAACCTTCTAGAGGACGTGCGAGAACTGGGAGCTGGCGAGGAGGCC 300
QY 301 ACCAAGACAGCGCTGCGAGGCTGCTGCGCACTTGTGCGAGTGCCTCCTCGCGGG 360
DB 301 ACCAAGACAGCGCTGCGAGGCTGCTGCGCACTTGTGCGAGTGCCTCCTCGCGGG 360
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DB 661 AAATGGAACAGAGCGGCTGAAGAGAAAGTGGCGAGAGATGGCTCTCTTGGAAAG 720
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Db 1021 ATGAAGGCTGGCAAGCCCATCACCAGAGG 1050

RESULT 8

US-10-217-745-3
; Sequence 3, Application US/10217745
; Patent No. 6838275
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilgowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6838275el Human G-Coupled Protein Receptor Kinases and
; TITLE OF INVENTION: Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/10/217,745
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US/09/802,117
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-217-745-3

Query Match 63.1%; Score 1046.8; DB 4; Length 1062;
Best Local Similarity 99.8%; Pred. No. 5.8e-259;
Matches 1048; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGTGGACATGGGGCCCTGGACAACTGATCGCAACACCGCCCTACTGCGAGCCCGG 60
Db 1 ATGTGGACATGGGGCCCTGGACAACTGATCGCAACACCGCCCTACTGCGAGCCCGG 60
QY 61 AAGCCCTCGACTGCGACAGCAAGAGCTGCAAGCGCGCGGCTAGCCTGGCCCTGCC 120
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Db 781 AAGACCCATCTCTGCTGTGATGAGCTGATGATGGGGAGACCTCAAGTTCACATC 840
QY 841 TACAACGTGGGACGCGTGGCTGGACATGAGCGGGTGTATCTTACTCGGCCAGATA 900
Db 841 TACAACGTGGGACGCGTGGCTGGACATGAGCGGGTGTATCTTACTCGGCCAGATA 900
QY 901 GCCTGTGGATGCTGACACTCCATGAACTCGGCTATGCTATCGGACATGAGCCTGAG 960
Db 901 GCCTGTGGATGCTGACACTCCATGAACTCGGCTATGCTATCGGACATGAGCCTGAG 960
QY 961 AATGTGCTTCTGGATGACCTCGCAACTGCAAGTGTATCTGACCTGGGCTGGCCGTGAG 1020
Db 961 AATGTGCTTCTGGATGACCTCGCAACTGCAAGTGTATCTGACCTGGGCTGGCCGTGAG 1020
QY 1021 ATGAAGGCTGGCAAGCCCATCACCAGAGG 1050
Db 1021 ATGAAGGCTGGCAAGCCCATCACCAGAGG 1050

RESULT 9

US-09-738-894A-3
; Sequence 3, Application US/09738894A
; Patent No. 6331423
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000636
; CURRENT APPLICATION NUMBER: US/09/738,894A
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 36651
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(36651)
; OTHER INFORMATION: n = A,T,C or G
US-09-738-894A-3

Query Match 37.2%; Score 617.4; DB 3; Length 36651;
Best Local Similarity 96.8%; Pred. No. 6.6e-148;
Matches 630; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 ATGTGGACATGGGGCCCTGGACAACTGATCGCAACACCGCCCTACTGCAAGGCCCGG 60
Db 2076 ATGTGGACATGGGGCCCTGGACAACTGATCGCAACACCGCCCTACTGCAAGGCCCGG 2135

QY 61 AAGCCCTCGGACTGCGACAGCAAGAGGTGCAAGCGCGCGCGCTAGCCTGCCCC 120
DB 2136 AAGCCCTCGGACTGCGACAGCAAGAGGTGCAAGCGCGCGCGCTAGCCTGCCCC 2195
QY 121 GGGCTGCAAGGCTGCGCGAGCTCGCGCAGAGCTGCTCCGAACTTCCACAGCCTGTGT 180
DB 2196 GGGCTGCAAGGCTGCGCGAGCTCGCGCAGAGCTGCTCCGAACTTCCACAGCCTGTGT 2255
QY 181 GAGCAGCAGCCCATCGGTGCGCGCTCTTCCGTGACTTCTAGCCACAGTGCACAGTTC 240
DB 2256 GAGCAGCAGCCCATCGGTGCGCGCTCTTCCGTGACTTCTAGCCACAGTGCACAGTTC 2315
QY 241 CGCAAGCGCGCAACTTCTTAGAGAGAGCTGCGAGAACTGGGAGCTGGCGAGAGGAGCCC 300
DB 2316 CGCAAGCGCGCAACTTCTTAGAGAGAGCTGCGAGAACTGGGAGCTGGCGAGAGGAGCCC 2375
QY 301 ACCAAGACAGCGCGCTCGAGGGCTGGTGGCCACTTGTGGAGTGGCCCCGGGG 360
DB 2376 ACCAAGACAGCGCGCTCGAGGGCTGGTGGCCACTTGTGGAGTGGCCCCGGGG 2435
QY 361 AACC CGCAACCTTCTCAGCGAGCGCTGGCCACCAAGTGCCAGCAGCCACCACTGAG 420
DB 2436 AACC CGCAACCTTCTCAGCGAGCGCTGGCCACCAAGTGCCAGCAGCCACCACTGAG 2495
QY 421 GAAAGCGAGTGGCTGAGTGCAGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGAAGAG 480
DB 2496 GAAAGCGAGTGGCTGAGTGCAGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGAAGAG 2555
QY 481 CAGCCCTTAAAGGATTTCTGACCAAGTACTTCTAGCAAGTTCAGAGTCTGGGAAAGGT 540
DB 2556 CAGCCCTTAAAGGATTTCTGACCAAGTACTTCTAGCAAGTTCAGAGTCTGGGAAAGGT 2615
QY 541 TTCGAGATGCAACCAAGTGTGCGCTCAGGTGAAAACACTGGGAAAGGT 600
DB 2616 TTCGAGATGCAACCAAGTGTGCGCTCAGGTGAAAACACTGGGAAAGGT 2675
QY 601 GGTTTGGGAGGTATGTGCGCTCAGGTGAAAACACTGGGAAAGGT 651
DB 2676 GGTTTGGGAGGTATGTGCGCTCAGGTGAAAACACTGGGAAAGGT 2726

RESULT 10

US-09-964-469-3
; Sequence 3, Application US/09964469
; Patent No. 6579709
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THERIOF
; FILE REFERENCE: CL000636DIV
; CURRENT APPLICATION NUMBER: US/09/964,469
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 60/208,331
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: 09/738,894
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 36651
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(36651)
; OTHER INFORMATION: n = A,T,C or G

US-09-964-469-3

Query Match 37.2%; Score 617.4; DB 4; Length 36651;
Best Local Similarity 96.8%; Pred. NO. 6.6e-148;
Matches 630; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 ATGTGGACATGGGGGCCCTGGAACAACCTGATGCAACACACCGCTACCTGAGGCCCGG 60
DB 2076 ATGTGGACATGGGGGCCCTGGAACAACCTGATGCAACACACCGCTACCTGAGGCCCGG 2135
QY 61 AAGCCCTCGGACTGCGACAGCAAGAGCTGCGAGCGCGCGCGCTAGCCTGCCCC 120
DB 2136 AAGCCCTCGGACTGCGACAGCAAGAGCTGCGAGCGCGCGCGCTAGCCTGCCCC 2195
QY 121 GGGCTGCAAGGCTGCGCGAGCTCGCGCAGAGCTGCTCCGAACTTCCACAGCCTGTGT 180
DB 2196 GGGCTGCAAGGCTGCGCGAGCTCGCGCAGAGCTGCTCCGAACTTCCACAGCCTGTGT 2255
QY 181 GAGCAGCAGCCCATCGGTGCGCGCTCTTCCGTGACTTCTAGCCACAGTGCACAGTTC 240
DB 2256 GAGCAGCAGCCCATCGGTGCGCGCTCTTCCGTGACTTCTAGCCACAGTGCACAGTTC 2315
QY 241 CGCAAGCGCGCAACTTCTTAGAGAGAGCTGCGAGAACTGGGAGCTGGCGAGAGGAGCCC 300
DB 2316 CGCAAGCGCGCAACTTCTTAGAGAGAGCTGCGAGAACTGGGAGCTGGCGAGAGGAGCCC 2375
QY 301 ACCAAGACAGCGCGCTCGAGGGCTGGTGGCCACTTGTGGAGTGGCCCCGGGG 360
DB 2436 AACC CGCAACCTTCTCAGCGAGCGCTGGCCACCAAGTGCCAGCAGCCACCACTGAG 2495
QY 421 GAAAGCGAGTGGCTGAGTGCAGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGAAGAG 480
DB 2496 GAAAGCGAGTGGCTGAGTGCAGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGAAGAG 2555
QY 481 CAGCCCTTAAAGGATTTCTGACCAAGTACTTCTAGCAAGTTCAGAGTCTGGGAAAGGT 540
DB 2556 CAGCCCTTAAAGGATTTCTGACCAAGTACTTCTAGCAAGTTCAGAGTCTGGGAAAGGT 2615
QY 541 TTCGAGATGCAACCAAGTGTGCGCTCAGGTGAAAACACTGGGAAAGGT 600
DB 2616 TTCGAGATGCAACCAAGTGTGCGCTCAGGTGAAAACACTGGGAAAGGT 2675
QY 601 GGTTTGGGAGGTATGTGCGCTCAGGTGAAAACACTGGGAAAGGT 651
DB 2676 GGTTTGGGAGGTATGTGCGCTCAGGTGAAAACACTGGGAAAGGT 2726

RESULT 11

US-08-464-954A-2
; Sequence 2, Application US/08464954A
; Patent No. 6255069
; GENERAL INFORMATION:
; APPLICANT: BENOVIC, JEFFREY L.; GOMEZ, JORGE; KUNAPULI,
; APPLICANT: PRIYA
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF G PROTEIN-COUPLED RECEPTOR
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jane Massey Licata, Esq.
; STREET: Woodland Falls Corporate Park
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,954A
; FILING DATE: Herewith

```

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076,084
; FILING DATE: June 11, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: JEFF-0118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2848
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; ANTI-SENSE: NO
; US-08-464-954A-2

Query Match      25.3%; Score 419.8; DB 3; Length 2848;
Best Local Similarity 56.2%; Pred. No. 1.3e-97;
Matches 891; Conservative 0; Mismatches 682; Indels 12; Gaps 5;

QY 15 GGCCTTGGACAACTGATCGCCCAACACCGCCTTACCTGCAAGGCCCGGAAGCCCTCGGACTG 74
DB 65 GGAGCTCGAGAACATCGTAGCGAAACACGGTGTCTACTCAAGGCCCGGGAAGGTGGCGGTGG 124
QY 75 CGACAGCAAAG---AGCTGACGGCGGGCGGTAGCTGGCCCTTGGCCGGGCTGCAGGG 131
DB 125 AAATCGCAAGCAAAAGCAAGAAATGGCGGCAGATGCTCCAGTTCCCTCAGCATCAGCCA 184
QY 132 CTGCGCGGAGCTCCGCCAGAACTGCTCCCTGAACTTCCACAGCCCTGTGTAGCGACGCC 191
DB 185 GTGCGAAGAGCTGCGGCTCAGCTCGAGCGTGACTATCACAGCCCTGTGCGAGCGCGCAGC 244
QY 192 CATCGGTGCGCCCTCTTCCTCGTACTTCTAGCCACAGTGGCCCAAGTTCCTCCGCAAGCGGC 251
DB 245 CATGGGCGCTGTCTTCGAGAGTCTGTGCGCAGAGCGCGAGCTGAGCGCGTGGT 304
QY 252 AACCTTCTAGAGAGCTGCGAACTGGGAGCTGGCCGAGAGGAGGCCACCAAGAGCAG 311
DB 305 CGCCTTCTCGTGGATGGGCTGGCGAGTATGAAGTGAACCCCGGATGACAAAGCGGAAGGCATG 364
QY 312 CGCGCTGACAGGGCTGGTGGCCACTTGTGCGAGTGGCCCTGCGCGGGAACCCGCAACC 371
DB 365 TGGCGGACAG---TAAAGCAGAAATTTCTGAGCCACACAGGCTCTGACCTCATCCCTGA 421
QY 372 CTCTCTAGCCAGCGCGTGGCCACCAAGTGGCCAGCAGCCACCACTGAGGAAGAGCGAGT 431
DB 422 GGTCCCGCGCAGCTGGTGACGAAC-TGCACCCAGCGGCTGAGCAGGTCCTCTGCAAG 480
QY 432 GGCTCAGTACGCTGCGCAAGCTGAGGCGCATGGCTTTCTTTCAGAGCAGCCCTTTAA 491
DB 481 ACCTTTTCCAGGAACCTACCCCGCTGA---CCACAGTACCTGAGCGTGGCCCTTTTGC 538
QY 492 GGATTTCTGTGACAGCGCTTCTAGACAAGTTTCTGAGTGGAACTCTTCGAGATGCA 551
DB 539 CGACTACTCTGACAGCATCTACTTCAACCGTTTCTGAGGTGGAAGTGGCTGGAAAGGCA 598
QY 552 ACCAGTGTGACAAAGTACTTCACTGAGTTGAGTGTGCTGGGGAAGGTGGTTTGGGGA 611
DB 599 GCCAGTGACCAAAACACTTCAGGCAATACCGAGTCTCTGGGCAAGGTGGCTTTGGGA 658
QY 612 GGTATGCGCTGAGGTGAAACACTGGGAAGATGTATGCTGTGTAAGAACTGGACAA 671
DB 659 GGTGTGCGCTTCCAGGTGCGGGCCACAGGTAAAGATGTATGCTGTGCAAGAGCTAGAGAA 718
QY 672 GAAGCGGTGGAAGAAAGGTGGCGAAGATGCTCTCTTGGAAAGGAAATCTTGA 731
DB 719 AAAGCGGATCAAGAACCGGAAGGGAGCCATGCGCTGAAACGAGAAAGCATCTTGA 778
QY 732 GAAGGTGACAGCCCTTTTCATTGTCTCTCTGCGCTATGCCCTTTTGAGACAAAGCCCATCT 791

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DB 779 GAAAGTGAACAGTAGGTTTGTAGTGAGCTTGGCCCTACGCCCTATGAGCAAGGAGCGCCT 838
QY 792 CTGCTTGTGATGAGCCTGATGAATGGGGAGAGCCTCAAGTTTCCACATCTTCAAGCTGGG 851
DB 839 GTGCTGTGTGCTGACACTGATGAACGGGGGCGACCTCAAGTTTCCACATCTTCAACATGGG 898
QY 852 CACCGTGGCTGGACATGAGCGGGGTGATCTTTTACTCGGCCAGATAGCCTGTGGGAT 911
DB 899 CCAGCTGGCTTCCCGAAGCGCGGGCGGCTTCTACGCCCGGAGATCTCTGTGGCT 958
QY 912 GCTCACCTCCATGAACCTCGGCATCGTCTATCGGGACATGAAGCCTGAGATGTGCTTCT 971
DB 959 GGAGGACCTGCACCGGGAGCGCATCGTGTACAGGACCTGAAGCCCAGAACTCTTCT 1018
QY 972 GGATGACCTCGGCAACTGCGAGTTTATCTGACCTGGGGCTGGCCCTGAGATGAAGGGTGG 1031
DB 1019 GGATGACCGACGGCCACATCCGCATCTCTGACCTGGGACTAGCTGTGATGTGCCCCGAGG 1078
QY 1032 CAAGCCCATCACCCAGAGGGCTGGAAACCAATGGTTTACATGGCTCTCGATCCTTAATGGA 1091
DB 1079 CCAGACCATCAAGGGGCTGTGGGCACCGTGGGTTTACATGGCTCCGAG---GTGGTGA 1135
QY 1092 AAAGTTAAGTTATTCTTATCCTGTGACTTGGTTTGCATGGGATGSCAGCATTTATGAAT 1151
DB 1136 GAATGAACGGTACAGCTTACAGCCCTGACTGTGGGCGCTCGGCTGCCTCTGTACGAGAT 1195
QY 1152 GGTGTGTGGAGAACACCATTTCAAGATTTCAAGGAAAGGTCAGTAAAGAGATCTGAA 1211
DB 1196 GATCACAGGCGAGTCGCCCTTCCAGCAGAGAGAAAGAAATCAAGCGGGAGGAGTGA 1255
QY 1212 GCAAAGAACTCTGCAAGACGAGGTCAAAATCCAGCATGATAACTTTCACAGAGGAAGCAA 1271
DB 1256 CGGCTGTGAGAGAGTCCCGAGGAGTATTCGAGCGGTTTCCCGCGAGGCCCGCTC 1315
QY 1272 AGATATTTCAGGCTCTTCTTGGCTAAGAAACCAAGAACAGCTTAGGAAGCAGAGAA 1331
DB 1316 ACTTGTCTCAGCTCTCTGCAAGGACCCCTGCGCAACGCTGGGGTGTCTGGGGGCGAG 1375
QY 1332 GTCTGATGATCCAGGAAACATCATTTCTTTAAACGATCAACTTCTCGCTCGCTGGAGC 1391
DB 1376 TGCCCGCGAGGTGAAGAGCAGCCCCCTCTTTTAAAGACTGAACCTTCAAGCGGCTGGAGC 1435
QY 1392 TGGCTTAATTGAACCCCTTGTGCGCAGACCCCTTCAGTGGTTTATGCAAGACATCGC 1451
DB 1436 TGGATGCTGGAGCGCGCTTCAAGCTGACCCCGAGCCATTTACTGCAAGGATGTCT 1495
QY 1452 TGAATTTGATGATTTCTCTGAGGTTGCGGGGGTGGAAATTTGATGACAAAGATAGCAGTT 1511
DB 1496 GGACATTGAACAGTTCTCTACGGTCAAGGGCGTGGAGCTGGAGCTTACCGACAGCAGTT 1555
QY 1512 CTTCAAAACTTTGCGACAGGTGCTGTTCTTATAGCATGCGCAGGAGAAATTTATAGAAC 1571
DB 1556 CTACCAAGTTTGGCAGAGGAGTGTGCCCATCCCTGGCAGAACGAGATGGTGGAGAC 1615
QY 1572 GGGACTGTTTGAAGAACTGAATGAC 1596
DB 1616 CGAGTGTCTTCAAGAGCTGAATGTC 1640

```

RESULT 12

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US-08-221-817-12
; Sequence 12, Application US/08221817
; Patent No. 5532151
; GENERAL INFORMATION:
; APPLICANT: Chantry, David
; APPLICANT: Gray, Patrick W.
; APPLICANT: Hoeft, Merle F.
; TITLE OF INVENTION: A No. 5532151el G Protein-Coupled Receptor
; TITLE OF INVENTION: Kinase GRK6
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

```


; ADDRESSEE: Botun
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/221,817
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/123,932
 ; FILING DATE: 17 SEP 1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 553215land, Greta E.
 ; REGISTRATION NUMBER: 35,302
 ; REFERENCE/DOCKET NUMBER: 31981
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 474-6300
 ; TELEFAX: (312) 474-0448
 ; TELEX: 25-3856
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2204 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 31..1758
 ; US-08-221-817-12

Query Match 25.2%; Score 418.2; DB 1; Length 2204;
 Best Local Similarity 56.2%; Pred. No. 2.9e-97;
 Matches 890; Conservative 0; Mismatches 683; Indels 12; Gaps 5;

Qy	15	GGCCCTGGACAACTGATGCGCAACACCGCCTACTGACGAGCCCGGAAGCCCTCGGACTG	74
Db	33	GGAGCTCGAAGACATCGTAGCAACACCGGTGCTACTCAAGGCCCGGAAGGTGGCGTGG	92
Qy	75	CGACAGCAAG---AGCTGCAGCGCGGGGGGTAGCTGGCCCTGCCCGGGCTGCAAGG	131
Db	93	AAATCGCAAGGCCAAGCAAGAAATGGCGGCAGATGTCTCCAGTTCCCTCAATCAGCCA	152
Qy	132	CTGCGCGGAGCTCCGCGCAAGCTGTCTCTGAACCTTCCACAGCCTGTGTGACGACGAGCC	191
Db	153	GTGCGAAGAGCTGGCGCTCAGCTCGAGGTGACTATCACGCCCTGTGGAGCGGCACGG	212
Qy	192	CATCGGTCCGCGCTCTTCCTGCTGACTTCTAGCCACAGTGGCCACCGTTCGCAAGCGGCG	251
Db	213	CATTGGCGCGCTGTGTTCCGAGAGTCTGTGCCACGAGCGGAGCTGAGCGCTGGCT	272
Qy	252	AACCTTCTAGAGACGTGCAGAACTGGGAGCTGGCGAGGAGGACCCACCAAGACAG	311
Db	273	CGCCTTCTGGATGGGTGGCGAGTATGAAGTGACCCCGGATCAAGCGGAAGGCATG	332
Qy	312	CGCGCTGAGGGGCTGGTGGCCACTTGTGCGAGTGCCTGCCCGCGGGAACCCGCAACC	371
Db	333	TGGGCGGACG---TAACGCAAGATTTCTGAGCCACAGGGTCTTGACCTCATCCCTGA	389
Qy	372	CTTCTCAGCCAGCGCGTGGCCACCAAGTGCCAAAGCAGCACCACTCAGGAGAGAGCGAGT	431
Db	390	GGTCCCGCGCAGCTGGTGAACGAC-TGCACCCAGCGGCTGGAGCAGGGTCCCTCGCAAG	448
Qy	432	GGCTGAGTGACGCTGCGCAAGGCTGAGCCATGCGTTTCTTGGCAAGAGCAGCCCTTTAA	491
Db	449	ACCTTTTCCAGGAATCAACCCGCGCTGA---CCACAGTAGTACCTGAGCGTGGCCCTTTTGC	506

Qy	492	GGATTTCTGACACGCGCTTCTACGACAAAGTTTCTGACGTGGAACATCTTTCGAGATGA	551
Db	507	CGACTACCTCGACAGCATCTACTTCAACCGTTTCTGACGTGGAAGTGGCTGGAAGGCA	566
Qy	552	ACCAGTGTGACAGAGTACTTCACTGAGTTCAGAGTGTGGGGAAGGTGGTTTGGGGA	611
Db	567	GCCAGTGACCAAAACACCTTTCAGGCAATACCGAGTCTTGGGTAAAGGTGGCTTTGGGGA	626
Qy	612	GATATGTCCCTCCAGGTGAAACACCTGGGAAGATGTATGCTCTGAAGAACTGACAA	671
Db	627	GGTGTGCGCTGCCAGGTGCGGGCCACAGGTAAAGATGTATGCTCTGCAAGAGCTAGAGAA	686
Qy	672	GAGCGGTGAAAGAAAGGTGGCGAAGATGGCTCTTTGGAAAAAGAAATCTTGA	731
Db	687	AAAGCGGATCAAGAAAGCGGAAGGCGCATGGCGCTGAACGAGAAGCAGATCTCTGA	746
Qy	732	GAAGTCAAGCGCTTTCATTGTCTCTCTGCGCTATGCTTGTGAGCAAGACCATCT	791
Db	747	GAAGTGAACAGTAGTGTGTGAGCTTGGCCCTACGCTTATGAGCAAGGACGCGCT	806
Qy	792	CTGCTTCTCATGAGCTGATGAATGGGGGAGACCTCAAGTTTCCACATCTACAAGTGG	851
Db	807	GTGCTGTGTGACACTGATGAAAGGGGGGCGACCTCAAGTTTCCACATCTACCAATGG	866
Qy	852	CACGCTGGCTTGGACATGAGCCGGGTGATCTTTTATCTGGGCCAGATAGCTGTGGAT	911
Db	867	CGAGCTGGCTTCCCGAAGCGCGGGCGCTCTTCTACGCGCGCGAGATCTGTGTGGCT	926
Qy	912	GCTGCACTCATGAACTGCGGCATGCTATCGGACATGAGCTGAGCTGAGATGTCTTCT	971
Db	927	GGAGGACCTGCACCGGGAGCGCATGTGTACAGGACCTGAAGCCCGGAGAACATCTTGT	986
Qy	972	GGTGAACCTCGCAACTGACGTTATCTGACTGGGGCTGGCGCTGGAGATGAAGGGTGG	1031
Db	987	GGATGACCAACCGCCACATCCGATCTCTGACTGGAATAGTGTGCTGATGCTGCGAGGG	1046
Qy	1032	CAAGCCCATCACCGAGGGCTGGAAACCAATGGTTTACATGGCTCTGAGATCCTTAATGA	1091
Db	1047	CCAGACCATCAAGGGCGTGTGGGCACCGTGGGTTTACATGGCTCGGAG---GTGGTGA	1103
Qy	1092	AAAGTAAAGTTATCTCTATCTGTGAGTGTGGTTCCTGAGTGGATGAGATGAGATTA	1151
Db	1104	GAATGAACGTTACAGCTTTCAGCCCTGAGTGGTGGCGCTCGGCTGCTCTGTACAGAT	1163
Qy	1152	GTTTGTGACGACCAACCATTTCAAGATTTCAAGGAAAGGTCACTAAAGAGATCTGAA	1211
Db	1164	GATCGAGCCAGTCCGCTTTCAGCAGAGGAAGAGAGATCAAGCGGAGAGGATGGA	1223
Qy	1212	GCAAGAACTCTGCAAGACGAGGTCAAAATTCAGCATGATTAATCTTCAAGAGGAAGCAA	1271
Db	1224	GCGGCTGGTGAAGAGGTCCCGAGGAGTATTTCCGAGCGCTTTTCCCGCAGGCCGCTC	1283
Qy	1272	AGATATTTGAGGCTCTTCTTGGCTAAGAAACAGAGCAACGCTTAGGAGCAGAGAA	1331
Db	1284	ACTTTGTCTACAGCTCTCTCTCAAGGACCTTCCGAAACGCTGGGGTGTCTGGGGGCGAG	1343
Qy	1332	GTCTGATCATCCAGGAAACATCATTTCTTTAAACAGATCAACTTCTCGCTCGAAGC	1391
Db	1344	TGCCCGGAGGTGAAGAGACACCCCTCTTTAAGAGCTGAATCTTCAAGCGCTGGAGC	1403
Qy	1392	TGGCCTAAATTGAACCCCATTTGTGCCAGACCTTTCAGTGGTTTATGCCAAGACATCGC	1451
Db	1404	TGGCATGTGAGCGCGCTTCAAGCCTGACCCCGAGGCCATTTACTGCAAGGATGTCT	1463
Qy	1452	TGAATTAAGATTTCTCTGAGTTTGGGGGGTGAATTTGATGACAAAGATTAAGCAGTT	1511
Db	1464	GGACATTAACAGATTTCTTACGGTCAAGGGGGTGGAGCTGGAGCTCCGACAGGACTT	1523
Qy	1512	CTTCAAAACCTTTCGACAGGTGCTTCTATAGCATGGCAGGAAGAAATTTATAGAAC	1571
Db	1524	CTACAGAGTTTGGCCACAGGAGGTGTGCCCATCCCTTGGCAGAACGAGATGGTGGAGAC	1583

QY 1572 GGAGCTGTTTGAGGAACCTGAATGAC 1596
Db 1584 CGAGTCTTCCAGAGCTGATGTC 1608

RESULT 13

US-08-454-439-12
Sequence 12, Application US/08454439
Patent No. 5591618
GENERAL INFORMATION:
APPLICANT: Chantry, David
APPLICANT: Gray, Patrick W.
APPLICANT: Hoekstra, Merle F.
TITLE OF INVENTION: A No. 5591618el G Protein-Coupled Receptor
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,439
FILING DATE: 30-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,817
FILING DATE: 31-MAR-1994
APPLICATION NUMBER: 08/123,932
FILING DATE: 17 SEP 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5591618and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31981
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2204 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 31..1758

US-08-454-439-12
Query Match 25.2%; Score 418.2; DB 1; Length 2204;
Best Local Similarity 56.2%; Pred. No. 2.9e-97;
Matches 890; Conservative 0; Mismatches 683; Indels 12; Gaps 5;

QY 15 GSCCTTGACCAACCTGATCGCCCAACACCGCCTACTCTGACGCGCCGGAAGCCCTCGGACTG 74
Db 33 GGAGCTCGAGACATCGTAGCGACACCGTGTACTCAAGCCCGGAGAGTGGCGTGG 92
QY 75 GCACAGCAAG---AGCTGCGCGCGCGGTAGCCTGCGCCCTGCGCGGCTGCAGGG 131
Db 93 AAATCGCAAGGCAAAAGCAAGAAATGCGCGCAGATGCTCCAGTTCCCTCATCAGCCA 152
QY 132 CTGGCGGAGCTCCGCGAGAGCTGCTCCCTGAACTTCCAGCTGTGTGAGGAGCGCC 191

Db 153 GTGCGAAGAGCTGGGCTCAGCCTCGAGCGTGACTATCAGACCTGTGTCGAGCGGCACCG 212
QY 192 CATCGGTGCGCGCCTCTTCCTGCTGACTTCCTTAGCCACAGTGCCTCAGTTCCTCCAGAGCGGC 251
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QY 252 AACCTTCTAGAGAGCTGAGAGTGGAGCTGGCCGAGGAGGAGGCCACCAAGAGCAG 311
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Db 333 TGGGCGGACG---TAACGCGAGATTTCTGAGCCACACGCGTCTGACCTTATCCCTGA 389
QY 372 CTTCTGACGCGCGCTGGCCACCAAGTGCACAGAGCCACCACTGAGGAGAGCGAGT 431
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QY 432 GGCTGCAGTGACGCTGCGCAAGGCTGAGGCGCATGGCTTTCTTTCGCAAGCAGCAGCCCTTAA 491
Db 449 ACCTTTCCAGGAACCTCACCGCGCTGA-CCACAGATACCTGAGCGTGGCCCCCTTTGC 506
QY 492 GGATTTCTGACACGCGCTTTCTACGACAAAGTTTCTGAGTGGAACCTCTTCGAGATGCA 551
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QY 552 ACCAGTGTACAGAAAGTACTTCTGAGTTCAGAGTCTGCGGGAAGGTTGTTTGGGA 611
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QY 1572 GGGACTTTTGAAGAACTGAATGAC 1596
Db 1584 CGAGTCTTCCAGAGCTGAATGTC 1608

RESULT 14

PCT-US94-10487-12
; Sequence 12, Application PC/TUS9410487
; GENERAL INFORMATION:
; APPLICANT: ICOS Corporation
; TITLE OF INVENTION: A Novel G Protein-Coupled Receptor
; TITLE OF INVENTION: Kinase GRK6
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESS: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10487
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/221,817
; FILING DATE: 31 MAR 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/123,932
; FILING DATE: 17 SEP 1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/31981
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2204 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31..1758
PCT-US94-10487-12

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Best Local Similarity 56.2%; Pred. No. 2.9e-97;
Matches 890; Conservative 0; Mismatches 683; Indels 12; Gaps 5;
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QY 75 CGACAGCAAAAG---AGCTGCAGCGCGCGCGCTAGCGCTGCGCCCTGCGCGGCTGACGG 131
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QY 132 CTGCGCGAGCTCGCCAGAACGCTGTCTGTAACCTTCCACAGCCTGTGTGAGCAGCAGCC 191
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QY 192 CATCGCTCGCGCTCTTCCGTGACTTCTTAGCCACAGTGCACGTTCCCGCAAGCGCGC 251
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QY 252 AACCTTCTAGAGGACGTGCAGAACTGGGAGCTGCGCGAGGAGGAGCCACCAAGAGCAG 311
Db 273 CGCCTTCTGATGGGTGGCGGATGATGAGTGAACCCCGATGACAAGCGGAGGCGATG 332
QY 312 CGCGCTGACGGGCTGTGGCCACTTGTGCGAGTGCCTGCCCCGGGGAACCCGCAACC 371
Db 333 TGGCGCGCACG---TAAACGACAGAAATTTCTGAGCCACACCGGCTCTGACCTCATCCTGA 389
QY 372 CTTCTCTAGCAGCGCGCTGCGCCACCAAGTGCACAGCAGCCACCACTGAGGAGAGCGAGT 431
Db 390 GGTCCCCCGGAGCTGTGTGAGAAC-TGCACCCAGCGGCTGGAGCAGGCTCCCTGCAAG 448
QY 432 GGCTGCAGTGAAGCTGCGCAAGGCTGAGGCGCATGGCTTTCTTGAAGAGCAGCCCTTTAA 491
Db 449 ACCTTTTCCAGGAATCAACCGGCTGA-CCCACAGATACCTGAGCGTGGGCCCTTTGC 506
QY 492 GGATTTCTGACAGCGCTTCTACGACAAGTTTCTGCAAGTGGAAACTCTTCGAGATGCA 551
Db 507 CGACTACTCTGACAGCATCTACTTCAACCGTTTCTGCAAGTGGAAAGTGGCTGGAAAGCA 566
QY 552 ACCAGTGTACAGCAAGTACTTCACTGAGTTCAGAGTGTGCGGGAAGGTGTTTGGGGA 611
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Db 627 GGTGTGCGCTGCGAGGTGCGGCGCACAGGTAAATGTATGCTGCAAGAGCTAGAGAA 686
QY 672 GAAGCGCTGAAGAAAGAGGTGCGAGAGATGGCTCTCTTTGAAAAAGGAAATCTTGA 731
Db 687 AAAGCGGATCAAGAAAGCGGAAAGGGAGGCCATGGCGCTGAACGAGAGCAGATCCTGGA 746
QY 732 GAAGTTCAGCAGCCCTTTCTTGTCTCTCTGGCCTATGCTTTCGAGCAGAGACCCATCT 791
Db 747 GAAAGTGAACAGTAGGTTTGTAGTGAGCTTGGCCCTACGCCCTATGAGACCAAGGAGCGCCT 806
QY 792 CTGCTTGTATGAGCTGATGAATGGGGAGAGCTCAAGTTTCCACATCTACAACGTGG 851
Db 807 GTGCTGTGCTGACATGATGAAGGGGGGAGCCTCAAGTTTCCACATCTACCATGCG 866
QY 852 CACGCTGTGGCTGGACATGAGCGCGGTGATCTTTTACTCGGCCCAGATGAGCTGTGGAT 911
Db 867 CCAGGCTGGCTTCCCGAAGCGCGGCGCTCTTCTAGCGCGCGGAGATCTGCTGTGGCT 926
QY 912 GCTGCACCTCCATGAACCTCGGCATCGTCTATCGGGACATGAGCCTGAGATGTGCTTCT 971
Db 927 GGAGGACCTGCACCGGGAGCGCATCGTGTACAGGGACCTGAAGGCCCGGAGAACATCTTGTCT 986

QY 972 GGATGACCTCGGCAACTCGAGGTTATCTGACCTGGGGCTGGCGTGAGATGAAGGGTG 1031
Db 987 GGATGACCGGCAATCGGATCTCTGACCTGGGACTAGCTGTGTCGCCAGGG 1046
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QY 1092 AAAGTAAGTATTCTTCTCTGTCGAGCTGGTTTCCATGGGATCGAGATTTTGAAT 1151
Db 1104 GAATGAACGGTACAGCTTCAGCCCTGACTGGTGGCGCTCGGCTGCTCTGACGAT 1163
QY 1152 GGTGTGTCGACGAACACCAATCAAGATTACAAAGAAAGTCAAGTAAGAGATCTGA 1211
Db 1164 GATCGAGCGAGTCCGCTTCCAGCAGAGGAAGAAAGATCAAGCGGAGAGGTGA 1223
QY 1212 GCAAGAACTCTGCAAGAGAGGTCAAAATCCAGCATGATACTTCAAGAGAGCAAA 1271
Db 1224 GCGGCTGGTGAAGGAGGTCGCGAGGATTTCCGAGCGCTTTCCCGCAGGCCGCTC 1283
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Db 1284 ACTTGTCTCAGAGCTCTCTGCAAGGACCTCGCGAACGCTGGGGTGTGTTGGGGCAG 1343
QY 1332 GTCTGATGATCCAGGAAACATCATTTCTTTAAACGATCACTTTCTCGCTCGAAGC 1391
Db 1344 TGCCCGGAGGTGAAGGAGCACCCCTCTTTAAGAGCTGAATCAAGCGCTGGAGC 1403
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Db 1404 TGGCATGTGGAGCGCGCTTCAAGCCTGACCCCGAGCCATTTACTGCAAGGATTTCT 1463
QY 1452 TGAATTTGATGATTTCTCTGAGTTTCGGGGGTGGAATTTGATGACAAAGATAGCATT 1511
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QY 1512 CTTCAAAATTTGGCAGAGTGTCTTCTATAGCATGGCAGGAAGAAATTTATAGAAC 1571
Db 1524 CTACAGAAATTTGCCAGGAGTGTGCCATCCCTTGGCAGACGAGATGGTGAGAC 1583
QY 1572 GGGACTGTTGAGAACTGAATGAC 1596
Db 1584 CGAGTGTCTCAAGAGCTGAATGTC 1608

RESULT 15

US-08-221-817-21
Sequence 21, Application US/08221817
Patent No. 5532151
GENERAL INFORMATION:
APPLICANT: Chantry, David
APPLICANT: Gray, Patrick W.
APPLICANT: Hoekstra, Werle F.
TITLE OF INVENTION: A No. 5532151el G Protein-Coupled Receptor
TITLE OF INVENTION: Kinase GRK6
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,817
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/123,932
FILING DATE: 17 SEP 1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5532151and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31981
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 1983 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 13...1740
US-08-221-817-21

Query Match 23.9%; Score 395.8; DB 1; Length 1983;
Best Local Similarity 55.3%; Pred. No. 1.6e-91;
Matches 876; Conservative 0; Mismatches 697; Indels 12; Gaps 5;
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 11, 2005, 00:07:33 ; Search time 2175.58 Seconds
(without alignments)
4667.000 Million cell updates/sec

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Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 562332 seqs, 3060109652 residues

Total number of hits satisfying chosen parameters: 11324664

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1659	100.0	2198	13 US-10-044-205A-1	Sequence 1, Appli
3	1655.8	99.8	1662	17 US-10-311-034-45	Sequence 45, Appli
4	1655.8	99.8	1662	17 US-10-451-168-49	Sequence 49, Appli
5	1655.8	99.8	1662	19 US-10-788-197-22	Sequence 22, Appli
6	1655.8	99.8	2249	9 US-09-802-117-5	Sequence 5, Appli
7	1655.8	99.8	2249	14 US-10-217-745-5	Sequence 5, Appli
8	1655.4	99.8	1662	9 US-09-802-117-1	Sequence 1, Appli
9	1655.4	99.8	1662	14 US-10-217-745-1	Sequence 1, Appli
10	1654.2	99.7	1662	9 US-09-964-469-1	Sequence 1, Appli
11	1654.2	99.7	1662	16 US-10-425-962-1	Sequence 1, Appli

12	1589.8	95.8	1701	17	US-10-072-012-273	Sequence 273, App
13	1046.8	63.1	1062	9	US-09-802-117-3	Sequence 3, Appli
14	1046.8	63.1	1062	14	US-10-217-745-3	Sequence 3, Appli
15	617.4	37.2	36651	9	US-09-964-469-3	Sequence 3, Appli
16	617.4	37.2	36651	16	US-10-425-962-3	Sequence 3, Appli
17	423	25.5	1683	19	US-10-788-197-8	Sequence 8, Appli
18	423	25.5	1770	19	US-10-788-197-6	Sequence 6, Appli
19	418.2	25.2	2848	19	US-10-788-197-10	Sequence 2, Appli
20	418.2	25.2	2848	9	US-09-851-686-2	Sequence 2, Appli
21	418.2	25.2	2848	10	US-09-873-367C-142	Sequence 142, App
22	418.2	25.2	2848	17	US-10-159-856-4	Sequence 4, Appli
23	418.2	25.2	2848	19	US-10-843-641A-142	Sequence 142, App
24	407.4	24.6	1692	19	US-10-788-197-24	Sequence 24, Appli
25	400.6	24.1	2817	17	US-10-388-934-621	Sequence 621, App
26	379.4	22.9	2467	15	US-10-084-817-110	Sequence 110, App
27	377.8	22.8	1773	19	US-10-788-197-12	Sequence 12, Appli
28	377.8	22.8	2519	13	US-10-071-766-13	Sequence 13, Appli
29	374.6	22.6	2519	10	US-03-971-392-72	Sequence 72, Appli
30	373	22.5	2511	14	US-10-072-036-60	Sequence 60, Appli
31	373	22.5	2529	14	US-10-072-036-42	Sequence 42, Appli
32	373	22.5	2557	9	US-09-972-694-1	Sequence 1, Appli
33	373	22.5	2557	17	US-10-305-720-1298	Sequence 1298, Ap
34	373	22.5	2557	17	US-10-380-235-7	Sequence 7, Appli
35	373	22.5	2557	18	US-10-775-169-77	Sequence 77, Appli
36	373	22.5	2557	18	US-10-723-860-2591	Sequence 2591, Ap
37	372.2	22.4	2558	18	US-10-723-860-6729	Sequence 6729, Ap
38	368.2	22.2	2557	9	US-09-851-686-1	Sequence 1, Appli
39	320.6	19.3	1641	19	US-10-788-197-16	Sequence 16, Appli
40	320.6	19.3	1737	15	US-10-325-430-2	Sequence 2, Appli
41	320.6	19.3	1737	19	US-10-788-197-18	Sequence 18, Appli
42	320.6	19.3	2017	19	US-10-677-983-8	Sequence 8, Appli
43	320.6	19.3	2113	16	US-10-325-430-1	Sequence 1, Appli
44	320.6	19.3	2113	19	US-10-677-983-7	Sequence 7, Appli
45	311.6	18.8	1503	19	US-10-788-197-14	Sequence 14, Appli

ALIGNMENTS

RESULT 1

US-10-044-205A-3
; Sequence 3, Application US/10044205A
; Publication No. US20020123464A1
; GENERAL INFORMATION:
; APPLICANT: KAPPELLER-LIBERMANN, Rosana
; APPLICANT: BANDARU, Rajasekhar
; TITLE OF INVENTION: 69087, 15821, and 15418, Methods and Compositions of Human Protei
; TITLE OF INVENTION: Uses thereof
; FILE REFERENCE: 10147-5201
; CURRENT APPLICATION NUMBER: US/10/044,205A
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/242,428
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: US 60/241,884
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/241,877
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1659
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-044-205A-3

Query Match 100.0%; Score 1659; DB 13; Length 1659;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1659; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGGACATGGGGGGCCCTGCACACCTGATCGCAACCGCTACTGCGAGCCCGG 60
DB 1 ATGTGGACATGGGGGGCCCTGCACACCTGATCGCAACCGCTACTGCGAGCCCGG 60

QY 61 AAGCCTCGGACTGCGACAGCAAGAGCTGCAGCGCGCGGCTAGCCTGGCCCTGCCC 120
Db 61 AAGCCTCGGACTGCGACAGCAAGAGCTGCAGCGCGCGGCTAGCCTGGCCCTGCCC 120
QY 121 GGGTGCAGGGCTGCGCGAGCTCGCGAGAGCTCGCGAGAGTGTCCCTGAACTTCCAAGCCTGTGT 180
Db 121 GGGTGCAGGGCTGCGCGAGCTCGCGAGAGTGTCCCTGAACTTCCAAGCCTGTGT 180
QY 181 GAGCAGCAGCCATCGGTGCGGCTCTTCCGTGACTTCCAGCAGCAGTGCACAGTTC 240
Db 181 GAGCAGCAGCCATCGGTGCGGCTCTTCCGTGACTTCCAGCAGCAGTGCACAGTTC 240
QY 241 CGCAGGCGGCAACCTTCTAGAGACGCTGCGAAGCTGGGAGCTGGCGAGGAGGAGCC 300
Db 241 CGCAGGCGGCAACCTTCTAGAGACGCTGCGAAGCTGGGAGCTGGCGAGGAGGAGCC 300
QY 301 ACCAAGACAGCGCTGCGAGGGCTGTGTGCGCACTTGTGAGTGTGCCCCCGGG 360
Db 301 ACCAAGACAGCGCTGCGAGGGCTGTGTGCGCACTTGTGAGTGTGCCCCCGGG 360
QY 361 AACCCGCAACCTTCTGAGCAGCGCTGCGCAAGCTGCGCAAGCTGCGCAAGCTGCG 420
Db 361 AACCCGCAACCTTCTGAGCAGCGCTGCGCAAGCTGCGCAAGCTGCGCAAGCTGCG 420
QY 421 GAAGAGCAGTGGCTGCAAGTGTGCGGAGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 480
Db 421 GAAGAGCAGTGGCTGCAAGTGTGCGGAGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 480
QY 481 CAGCCCTTTAAGATTTCTGACCAAGCTGCTTCTACGCAAGTGTGCGAGTGGAACTC 540
Db 481 CAGCCCTTTAAGATTTCTGACCAAGCTGCTTCTACGCAAGTGTGCGAGTGGAACTC 540
QY 541 TTGCGAGTCAACCAAGTGTGCGCAAGTGTGCGCAAGTGTGCGCAAGTGTGCGCAAG 600
Db 541 TTGCGAGTCAACCAAGTGTGCGCAAGTGTGCGCAAGTGTGCGCAAGTGTGCGCAAG 600
QY 601 GGTGTTGGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Db 601 GGTGTTGGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
QY 661 AAATGGAACAAGCGCTGGAAGAAAGTGGCGAGAGTGGCTCTCTTGGAAAG 720
Db 661 AAATGGAACAAGCGCTGGAAGAAAGTGGCGAGAGTGGCTCTCTTGGAAAG 720
QY 721 GAATCTTGGAGAGTCAAGCGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db 721 GAATCTTGGAGAGTCAAGCGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
QY 781 AAGACCCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
Db 781 AAGACCCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
QY 841 TACAAGTGGGACGGTGGCTGAGCATGAGCGGCTGATCTTTTACTCGGCCAGATA 900
Db 841 TACAAGTGGGACGGTGGCTGAGCATGAGCGGCTGATCTTTTACTCGGCCAGATA 900
QY 901 GCTGTGGATGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Db 901 GCTGTGGATGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
QY 961 AATGTCTTCTGATGACCTCGGCAACTGCAAGTGTATCTGACCTGGGGTGGCGTGGAG 1020
Db 961 AATGTCTTCTGATGACCTCGGCAACTGCAAGTGTATCTGACCTGGGGTGGCGTGGAG 1020
QY 1021 ATGAAGGGTGGCAAGCCATCACCGAGGGCTGGAACCAATGGTTTACATGGCTCTGAG 1080
Db 1021 ATGAAGGGTGGCAAGCCATCACCGAGGGCTGGAACCAATGGTTTACATGGCTCTGAG 1080
QY 1081 ATCTTAATGAAGTGAAGTATTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
Db 1081 ATCTTAATGAAGTGAAGTATTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
QY 1141 ATTTATGAATGGTGTGCTGGAAGCAACCAATTTCAAGAAAGGTGAGTAA 1200

Db 1141 ATTTATGAATGGTGTGCTGGAAGCAACCAATTTCAAGAAAGGTGAGTAA 1200
QY 1201 GAGGATCTGAAGCAAGAACTCTGCAAGAGAGGTCAAAATTCAGAGCATGATACTTACA 1260
Db 1201 GAGGATCTGAAGCAAGAACTCTGCAAGAGAGGTCAAAATTCAGAGCATGATACTTACA 1260
QY 1261 GAGGAACAAAGATATTTGCGAGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
Db 1261 GAGGAACAAAGATATTTGCGAGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
QY 1321 AGCAGAGAAAGTCTGATGATCCAGAGAAATCAATTTCTTTAAACGATCAACTTTCCT 1380
Db 1321 AGCAGAGAAAGTCTGATGATCCAGAGAAATCAATTTCTTTAAACGATCAACTTTCCT 1380
QY 1381 CGCTGGAAGTGGCTTAAATTTGAACCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
Db 1381 CGCTGGAAGTGGCTTAAATTTGAACCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
QY 1441 AAAGACATCGCTGAAATTTGATGATTTCTGAGGTTGCGGGGGTGGAAATTTGATGACAAA 1500
Db 1441 AAAGACATCGCTGAAATTTGATGATTTCTGAGGTTGCGGGGGTGGAAATTTGATGACAAA 1500
QY 1501 GATAGCAAGTCTTCAAAACTTTGCGACAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
Db 1501 GATAGCAAGTCTTCAAAACTTTGCGACAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
QY 1561 ATTATAGAAACGGGACTGTTTGAAGAACTGAACTGAACTGAACTGAACTGAACTGAACTG 1620
Db 1561 ATTATAGAAACGGGACTGTTTGAAGAACTGAACTGAACTGAACTGAACTGAACTGAACTG 1620
QY 1621 GAGGTAATTCATCAAGTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1659
Db 1621 GAGGTAATTCATCAAGTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1659

RESULT 2
US-10-044-205A-1
; Sequence 1, Application US/10044205A
; Publication No. US20020123464A1
; GENERAL INFORMATION:
; APPLICANT: KAPILLER-LIBERMAN, Rosana
; APPLICANT: BANDARU, Rajasekhar
; TITLE OF INVENTION: 69087, 15821, and 15418, Methods and Compositions of Human Protei
; FILE REFERENCE: 10147-52U1
; CURRENT APPLICATION NUMBER: US/10/044,205A
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/242,428
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: US 60/241,884
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/241,877
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 2198
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-044-205A-1

Query Match 100.0%; Score 1659; DB 13; Length 2198;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1659; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCTGGACATGGGGGCTTGGACAACTGATCGCCACACCGCTACTCTGAGCGCCGG 60
Db 291 ATGCTGGACATGGGGGCTTGGACAACTGATCGCCACACCGCTACTCTGAGCGCCGG 350
QY 61 AAGCCCTCGGACTGCGACAGCAAGAGGTGCGAGCGCGCGGCTAGCCTGCGCCCTGCCC 120
Db 351 AAGCCCTCGGACTGCGACAGCAAGAGGTGCGAGCGCGCGGCTAGCCTGCGCCCTGCCC 410

FILE REFERENCE: GP50039
CURRENT APPLICATION NUMBER: US/10/451,168
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: PCT/US01/49232
PRIOR FILING DATE: 2000-12-17
PRIOR APPLICATION NUMBER: 60/256,710
PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/257,048
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 60/260,482
PRIOR FILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: 60/264,922
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/266,797
PRIOR FILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/276,988
PRIOR FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 60/281,535
PRIOR FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 60/289,622
PRIOR FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 110
SOFTWARE: PaetSeq for Windows Version 4.0
SEQ ID NO 49
LENGTH: 1662
TYPE: DNA
ORGANISM: Homo sapiens
US-10-451-168-49

Query Match 99.8%; Score 1655.8; DB 17; Length 1662;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1657; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1	ATGTTGGACATGGGGCCCTGCACAACTGATCGCCAAACACCGCCCTACTCGCAGGCCGG	60
Db	1	ATGTTGGACATGGGGCCCTGCACAACTGATCGCCAAACACCGCCCTACTCGCAGGCCGG	60
Qy	61	AAGCCCTCGGACTGCGACAGCAAGAGCTGCGAGCGCGCGGTAGCCCTGCGCC	120
Db	61	AAGCCCTCGGACTGCGACAGCAAGAGCTGCGAGCGCGCGGTAGCCCTGCGCC	120
Qy	121	GGCTGCGAGGGTGGCGGAGCTCGCCGAGAGCTGCTGCACTTCGACAGCCCTGTGT	180
Db	121	GGCTGCGAGGGTGGCGGAGCTCGCCGAGAGCTGCTGCACTTCGACAGCCCTGTGT	180
Qy	181	GAGCAGCAGCCCATCGCTCGCGCCCTCTTCGCTGACTTCTAGCCACAGTGCACAGTTC	240
Db	181	GAGCAGCAGCCCATCGCTCGCGCCCTCTTCGCTGACTTCTAGCCACAGTGCACAGTTC	240
Qy	241	CGCAAGGGCGCAACCTTCTTAGAGGACGTGCGAGAACTGGGAGCTGGCGAGGAGGCC	300
Db	241	CGCAAGGGCGCAACCTTCTTAGAGGACGTGCGAGAACTGGGAGCTGGCGAGGAGGCC	300
Qy	301	ACCAAGACAGCGCGCTGAGGGGCTGTGGCCACTGTGCGAGTGGCCCTGCGCCCGGG	360
Db	301	ACCAAGACAGCGCGCTGAGGGGCTGTGGCCACTGTGCGAGTGGCCCTGCGCCCGGG	360
Qy	361	AACCGCAACCTTCTTAGAGGACGTGCGAGAACTGGGAGCTGGCGAGGAGGCCACTGAG	420
Db	361	AACCGCAACCTTCTTAGAGGACGTGCGAGAACTGGGAGCTGGCGAGGAGGCCACTGAG	420
Qy	421	GAAAGCGAGTGGCTGCACTGACGCTGCGCAAGGCTGAGGCCCATGGCTTTCTTGAAGAG	480
Db	421	GAAAGCGAGTGGCTGCACTGACGCTGCGCAAGGCTGAGGCCCATGGCTTTCTTGAAGAG	480
Qy	481	CAGCCCTTAAGGATTTCTGACAGCGCTTCTAGCAAGTTCCTGAGTGGAACTC	540
Db	481	CAGCCCTTAAGGATTTCTGACAGCGCTTCTAGCAAGTTCCTGAGTGGAACTC	540
Qy	541	TTGAGATGACACAGTGTGACAGTACTTCACTGAGTTCAGAGTGTCTGGGAAAGGT	600
Db	541	TTGAGATGACACAGTGTGACAGTACTTCACTGAGTTCAGAGTGTCTGGGAAAGGT	600

Qy	601	GGTTTGGGAGGTATGTGCCGTCCAGGTGAAACACCTGGGAAGATGTATGCCCTGTAA	660
Db	601	GGTTTGGGAGGTATGTGCCGTCCAGGTGAAACACCTGGGAAGATGTATGCCCTGTAA	660
Qy	661	AAACTGGACAAAGAGCGGCTGAAGAAAGAGTGGCGAAGAGATGGCTCTCTTTGAAAG	720
Db	661	AAACTGGACAAAGAGCGGCTGAAGAAAGAGTGGCGAAGAGATGGCTCTCTTTGAAAG	720
Qy	721	GAAATCTTTGGAGAAAGGTGAGAGAGGCTTTCATTTGTCTCTCTGGCCCTATGCTT	780
Db	721	GAAATCTTTGGAGAAAGGTGAGAGAGGCTTTCATTTGTCTCTCTGGCCCTATGCTT	780
Qy	781	AAGACCCATCTCTGCTTGTATGAGCCTGATGAATGGGGAGAGCTCAAGTTCCACATC	840
Db	781	AAGACCCATCTCTGCTTGTATGAGCCTGATGAATGGGGAGAGCTCAAGTTCCACATC	840
Qy	841	TACAACTGGGACGCGCTGAGCATGAGCGGGTGTCTTTTACTCTGGCCCCAGATA	900
Db	841	TACAACTGGGACGCGCTGAGCATGAGCGGGTGTCTTTTACTCTGGCCCCAGATA	900
Qy	901	GCCTGTGGATGTGTCACCTCCATGAACCTCGGCATCGTCTATCGGGACATGAAGCTGAG	960
Db	901	GCCTGTGGATGTGTCACCTCCATGAACCTCGGCATCGTCTATCGGGACATGAAGCTGAG	960
Qy	961	AATGTCTTCTGATGACCTCGGCAACTGCGAGGTTATCTGACCTGGGGTGGCCGTGAG	1020
Db	961	AATGTCTTCTGATGACCTCGGCAACTGCGAGGTTATCTGACCTGGGGTGGCCGTGAG	1020
Qy	1021	ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCTGAG	1080
Db	1021	ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCTGAG	1080
Qy	1081	ATCTTAATGGAAGGTAAGTTATTCCTATCTCTGGAAGTGGTTGCCATGGGATGCAGC	1140
Db	1081	ATCTTAATGGAAGGTAAGTTATTCCTATCTCTGGAAGTGGTTGCCATGGGATGCAGC	1140
Qy	1141	ATTTATGAATGGTTGTCGAGCAACACCATTCAGAGTTTCAAGAAAGGTTCAGTAA	1200
Db	1141	ATTTATGAATGGTTGTCGAGCAACACCATTCAGAGTTTCAAGAAAGGTTCAGTAA	1200
Qy	1201	GAGGATCTGAAGCAAGAACTCTGCAAGCAGAGTCAAAATTCAGAGTATGAATTCACA	1260
Db	1201	GAGGATCTGAAGCAAGAACTCTGCAAGCAGAGTCAAAATTCAGAGTATGAATTCACA	1260
Qy	1261	GAGGAAGCAAAAGATATTTGAGGCTCTTCTGCTTGAAGAAACCAAGAGCAACGCTTAGGA	1320
Db	1261	GAGGAAGCAAAAGATATTTGAGGCTCTTCTGCTTGAAGAAACCAAGAGCAACGCTTAGGA	1320
Qy	1321	AGCAGAGAAAGTCTGATGATCCCAAGGAAACATCATTTCTTTAAACGATCAACTTCCT	1380
Db	1321	AGCAGAGAAAGTCTGATGATCCCAAGGAAACATCATTTCTTTAAACGATCAACTTCCT	1380
Qy	1381	CGCTGGAGTGGCTTAATTTGAACCCCATTTGTCAGAGTGGCCAGAGTTCAGTGGTTATGCC	1440
Db	1381	CGCTGGAGTGGCTTAATTTGAACCCCATTTGTCAGAGTGGCCAGAGTTCAGTGGTTATGCC	1440
Qy	1441	AAAGACATCGCTGAAATTTGATGATTTCTGAGGTTTCGGGGGTGGAAATTTGATGACAAA	1500
Db	1441	AAAGACATCGCTGAAATTTGATGATTTCTGAGGTTTCGGGGGTGGAAATTTGATGACAAA	1500
Qy	1501	GATAGAGTCTTCAAAACCTTTGCGACAGGTGCTGTCTTATAGCATGGCAGAGAA	1560
Db	1501	GATAGAGTCTTCAAAACCTTTGCGACAGGTGCTGTCTTATAGCATGGCAGAGAA	1560
Qy	1561	ATTATAGAAAGGAGTGTGAGGAACTGAATGACCCCAACAGAGTTCAGGTTGTGAG	1620
Db	1561	ATTATAGAAAGGAGTGTGAGGAACTGAATGACCCCAACAGAGTTCAGGTTGTGAG	1620
Qy	1621	GAGGTAATTCATCCAGTCTGGCGTGTGTTGTTATTG	1659
Db	1621	GAGGTAATTCATCCAGTCTGGCGTGTGTTGTTATTG	1659

RESULT 5

US-10-788-197-22
; Sequence 22, Application US/10788197
; Publication No. US20050032125A1
; GENERAL INFORMATION:
; APPLICANT: OAKLEY, ROBERT H.
; APPLICANT: HUDSON, CHRISTINE C.
; TITLE OF INVENTION: CONSTITUTIVELY TRANSLOCATING CELL LINE
; FILE REFERENCE: NRK.108
; CURRENT APPLICATION NUMBER: US/10/788,197
; CURRENT FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: PCT/US03/14581
; PRIOR FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: 60/379,986
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: 60/401,698
; PRIOR FILING DATE: 2002-08-07
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 22
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-788-197-22

Query Match 99.8%; Score 1655.8; DB 19; Length 1662;

Best Local Similarity 99.9%; Pred. No. 0;
Matches 1657; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1	ATGTGGACATCGGGGCGCTGCAACACCTGATCGCAACACCGCTTACCTGAGCGCCCGG	60
DB	1	ATGTGGACATCGGGGCGCTGCAACACCTGATCGCAACACCGCTTACCTGAGCGCCCGG	60
QY	61	AGCCCTCGGACTGGACAGCAAGAGCTGCGCGCGCGCGCGCTAGCCTGCGCCCTGCC	120
DB	61	AGCCCTCGGACTGGACAGCAAGAGCTGCGCGCGCGCGCGCTAGCCTGCGCCCTGCC	120
QY	121	GGCTGCGAGGCTGCGCGAGCTCGCGCAAGAGCTGCTCCGAACTTCCACAGCCTGT	180
DB	121	GGCTGCGAGGCTGCGCGAGCTCGCGCAAGAGCTGCTCCGAACTTCCACAGCCTGT	180
QY	181	GAGCGACGCCCATCGGTGCGCGCTTCCGTGACTTCCAGCAAGTGCACAGTGC	240
DB	181	GAGCGACGCCCATCGGTGCGCGCTTCCGTGACTTCCAGCAAGTGCACAGTGC	240
QY	241	CGCAGGCGGCAACCTTCTAGAGACGTGCGAGAACTGGGAGCTGGCGAGGGAGCC	300
DB	241	CGCAGGCGGCAACCTTCTAGAGACGTGCGAGAACTGGGAGCTGGCGAGGGAGCC	300
QY	301	ACCAAGACAGCGCGCTGCGAGGCGTGGTGGCCACTTGTGCGAGTGCCTGCCCGGG	360
DB	301	ACCAAGACAGCGCGCTGCGAGGCGTGGTGGCCACTTGTGCGAGTGCCTGCCCGGG	360
QY	361	AAACCGCAACCTTCTCAGCAGCGCGTGGCCACCAAGTGCACAGCAGCCACTGAG	420
DB	361	AAACCGCAACCTTCTCAGCAGCGCGTGGCCACCAAGTGCACAGCAGCCACTGAG	420
QY	421	GAAGAGCGAGTGGTGCAGTACGCTGCGCAAGCTGAGGCGCATGGCTTCTTGAAG	480
DB	421	GAAGAGCGAGTGGTGCAGTACGCTGCGCAAGCTGAGGCGCATGGCTTCTTGAAG	480
QY	481	CAGCCCTTTAAGGATTTCTGACACAGCGCTTCTACGACAACTTCTCAGTGGAACTC	540
DB	481	CAGCCCTTTAAGGATTTCTGACACAGCGCTTCTACGACAACTTCTCAGTGGAACTC	540
QY	541	TTGAGATGCAACACAGTGTGAGCAAGTACTTCACTGAGTTTCTGAGTGTGGGAAAGGT	600
DB	541	TTGAGATGCAACACAGTGTGAGCAAGTACTTCACTGAGTTTCTGAGTGTGGGAAAGGT	600
QY	601	GGTTTGGGAGGTATGTCCTGCGTCCAGCTGGAACACTGGGAGATGATGCTGTGAAG	660
DB	601	GGTTTGGGAGGTATGTCCTGCGTCCAGCTGGAACAACTGGGAGATGATGCTGTGAAG	660

RESULT 6

US-09-802-117-5
; Sequence 5, Application US/09802117
; Publication No. US20020042503A1

QY	661	AACTGGCAAGAGCGGCTGAAGAAAGAGTGGCGAGAAAGATGGCTCTCTTGGAAAAG	720
DB	661	AACTGGCAAGAGCGGCTGAAGAAAGAGTGGCGAGAAAGATGGCTCTCTTGGAAAAG	720
QY	721	GAATCTTTGAGAAAGTTCAGAGCCCTTTCATTTCTCTCTGGGCTATGCTTGGAGAGC	780
DB	721	GAATCTTTGAGAAAGTTCAGAGCCCTTTCATTTCTCTCTGGGCTATGCTTGGAGAGC	780
QY	781	AAGACCCATCTCTGCTTGTATGAGCTGATGATGGGGGAGAGCCTCAAGTTCACATC	840
DB	781	AAGACCCATCTCTGCTTGTATGAGCTGATGATGGGGGAGAGCCTCAAGTTCACATC	840
QY	841	TACAAAGTGGGCGCGCTGACATGAGCGGGTATCTTTTACTTCGCGCCAGATA	900
DB	841	TACAAAGTGGGCGCGCTGACATGAGCGGGTATCTTTTACTTCGCGCCAGATA	900
QY	901	GCCTGTGGATGCTGCAACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG	960
DB	901	GCCTGTGGATGCTGCAACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG	960
QY	961	AATGTGCTTCTGGATGACCTCGGCAACTGCGAGTATCTGACCTGGGCTGGCGGTGAG	1020
DB	961	AATGTGCTTCTGGATGACCTCGGCAACTGCGAGTATCTGACCTGGGCTGGCGGTGAG	1020
QY	1021	ATGAAGGTGGCAAGCCCATCACCCAGAGGCTCGAAACCAATGTTACATGGCTCCTGAG	1080
DB	1021	ATGAAGGTGGCAAGCCCATCACCCAGAGGCTCGAAACCAATGTTACATGGCTCCTGAG	1080
QY	1081	ATCCTAATGAAAAAGTAAAGTTATTCCTATCTCTGGAATGGTTTGGCATGGGATGAGC	1140
DB	1081	ATCCTAATGAAAAAGTAAAGTTATTCCTATCTCTGGAATGGTTTGGCATGGGATGAGC	1140
QY	1141	ATTTATGAAATGGTGTGCGACGACCACTTCAAGATTTACAGAAAGAGTCAAGTAA	1200
DB	1141	ATTTATGAAATGGTGTGCGACGACCACTTCAAGATTTACAGAAAGAGTCAAGTAA	1200
QY	1201	GAGGATCTGAAGCAAGAACTCTCAAGACAGAGTCAAAATCCACAGATGATACTTACA	1260
DB	1201	GAGGATCTGAAGCAAGAACTCTCAAGACAGAGTCAAAATCCACAGATGATACTTACA	1260
QY	1261	GAGAAACAAAGATATTTGAGGCTCTTCTGCTTAAGAAACAGAGCAACGTTTAGGA	1320
DB	1261	GAGAAACAAAGATATTTGAGGCTCTTCTGCTTAAGAAACAGAGCAACGTTTAGGA	1320
QY	1321	AGCAGAGAAAGTCTGATGATCCAGGAAACATCACTTTCTTAAACGATCAACTTTCCT	1380
DB	1321	AGCAGAGAAAGTCTGATGATCCAGGAAACATCACTTTCTTAAACGATCAACTTTCCT	1380
QY	1381	CGCCTGGAAGCTGGCCTAAATTTGAACCCCAATTTGTGCGACAGCCCTTCAGTGGTTATGCC	1440
DB	1381	CGCCTGGAAGCTGGCCTAAATTTGAACCCCAATTTGTGCGACAGCCCTTCAGTGGTTATGCC	1440
QY	1441	AAAGACATGCTGAAATTTGATGATTTCTCTGAGGTTTCGGGGGGTGGAAATTTGATGACAA	1500
DB	1441	AAAGACATGCTGAAATTTGATGATTTCTCTGAGGTTTCGGGGGGTGGAAATTTGATGACAA	1500
QY	1501	GATAAGCAGTCTTCAAAACTTTCGACAGGCTGCTCTTCTATAGCATGCGCAGGAAGAA	1560
DB	1501	GATAAGCAGTCTTCAAAACTTTCGACAGGCTGCTCTTCTATAGCATGCGCAGGAAGAA	1560
QY	1561	ATTATAGAAACGGGACTGTTTGGAGAACTGAATGACCCCAACAGACCTACGGGTGTGAG	1620
DB	1561	ATTATAGAAACGGGACTGTTTGGAGAACTGAATGACCCCAACAGACCTACGGGTGTGAG	1620
QY	1621	GAGGTAATTCATCCAAAGTCTGGCGTGTGTTTATTG	1659
DB	1621	GAGGTAATTCATCCAAAGTCTGGCGTGTGTTTATTG	1659

GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6444456el Human G-Coupled Protein Receptor Kinases and Polynu
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/09/802,117
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/188,449
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq For Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2249
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-802-117-5

Query Match 99.8%; Score 1655.8; DB 9; Length 2249;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1657; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1	ATGTTGGACATGGGGGCTGGACAACTGATCGCCCAACACCGCTACCTGCGAGGCCCGG	60
Db	354	ATGTTGGACATGGGGGCTGGACAACTGATCGCCCAACACCGCTACCTGCGAGGCCCGG	413
Qy	61	AAGCCCTCGACTGCGACAGCAAAAGAGCTGACGCGCGCGCGTAGCCTGSCCTGCC	120
Db	414	AAGCCCTCGACTGCGACAGCAAAAGAGCTGACGCGCGCGCGTAGCCTGSCCTGCC	473
Qy	121	GGGCTGACAGGGTGGCGGAGCTCGCCAGAGCTGTCCCTGAACTTCCACAGCCTGTG	180
Db	474	GGGCTGACAGGGTGGCGGAGCTCGCCAGAGCTGTCCCTGAACTTCCACAGCCTGTG	533
Qy	181	GAGCAGCAGCCATCGGTGCGCGCTCTTCGTGATCTTCCAGCAGAGTGCACAGTTC	240
Db	534	GAGCAGCAGCCATCGGTGCGCGCTCTTCGTGATCTTCCAGCAGAGTGCACAGTTC	593
Qy	241	CGAAGCGGCAACCTTCTAGAGAGCTGAGAACTGGAGCTGGCGAGGAGGACCC	300
Db	594	CGAAGCGGCAACCTTCTAGAGAGCTGAGAACTGGAGCTGGCGAGGAGGACCC	653
Qy	301	ACCAAAGACAGCGCTGCGAGGGCTGTGGCCACTTGTGAGAGTGCCTGCCCGGGG	360
Db	654	ACCAAAGACAGCGCTGCGAGGGCTGTGGCCACTTGTGAGAGTGCCTGCCCGGGG	713
Qy	361	AACCGGCAACCTTCTCAGCAGCGCTGGCCACCAAGTGCCAAAGCAGCCCACTGAG	420
Db	714	AACCGGCAACCTTCTCAGCAGCGCTGGCCACCAAGTGCCAAAGCAGCCCACTGAG	773
Qy	421	GAAGAGCAGTGGCTGCAAGTGCAGCTGCGCAAGGCTGAGGCGCATGCTTCTTCAAG	480
Db	774	GAAGAGCAGTGGCTGCAAGTGCAGCTGCGCAAGGCTGAGGCGCATGCTTCTTCAAG	833
Qy	481	CAGCCCTTAAAGGATTTCTGACCAAGCGCTTCTACGACAAAGTTTCTGAGTGAAC	540
Db	834	CAGCCCTTAAAGGATTTCTGACCAAGCGCTTCTACGACAAAGTTTCTGAGTGAAC	893
Qy	541	TTGAGATGCAACCAAGTGCAGCAAGTACTTCACTGATTCAGAGTGTGGGAAAGGT	600
Db	894	TTGAGATGCAACCAAGTGCAGCAAGTACTTCACTGATTCAGAGTGTGGGAAAGGT	953
Qy	601	GGTTTGGGAGGTATGTCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	660
Db	954	GGTTTGGGAGGTATGTCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1013
Qy	661	AAACTGGCAAGAGCGCTGAAGAGAAAGAGTGGGAGAGAGTGGCTCTCTTGGAAAG	720
Db	1014	AAACTGGCAAGAGCGCTGAAGAGAAAGAGTGGGAGAGAGTGGCTCTCTTGGAAAG	1073
Qy	721	GAAATCTTTGGAGAGGTGACAGCCCTTTCATTTGCTCTGCGCTATGCTTTCGAGC	780

Db	1074	GAAATCTTTGGAGAGGTGACAGAGCCCTTTCAATGTCTCTCTGGGCTATGCTTTCGAGAC	1133
Qy	781	AAGACCCCATCTCTGCTTGTGATGAGCCTGATGAATGGGGAGAGCCTCAAGTTCCACATC	840
Db	1134	AAGACCCCATCTCTGCTTGTGATGAGCCTGATGAATGGGGAGAGCCTCAAGTTCCACATC	1193
Qy	841	TACAACGTGGGCAAGCGGTGGCTGACATGAGCCGGGTGATCTTTACTCGGCCAGATA	900
Db	1194	TACAACGTGGGCAAGCGGTGGCTGACATGAGCCGGGTGATCTTTACTCGGCCAGATA	1253
Qy	901	GCCTGTGGATGCTGCACCTCCATGAACCTCGGCATCGTCTATCGGGACATGAAGCTGAG	960
Db	1254	GCCTGTGGATGCTGCACCTCCATGAACCTCGGCATCGTCTATCGGGACATGAAGCTGAG	1313
Qy	961	AATGTGCTTCTGGATGACCTCGCAACCTGACAGTTTATCTGACCTGGGCTGSCCTGGAG	1020
Db	1314	AATGTGCTTCTGGATGACCTCGCAACCTGACAGTTTATCTGACCTGGGCTGSCCTGGAG	1373
Qy	1021	ATGAAGGTGGCAAGCCCATCACCAGAGGCTGGAACCAATGTTTACATGGCTCTGAG	1080
Db	1374	ATGAAGGTGGCAAGCCCATCACCAGAGGCTGGAACCAATGTTTACATGGCTCTGAG	1433
Qy	1081	ATCCTAATGGAAGGTAAGTTATTCTCTATCTGTGAGCTGTTTCCATGCGATGCGAGC	1140
Db	1434	ATCCTAATGGAAGGTAAGTTATTCTCTATCTGTGAGCTGTTTCCATGCGATGCGAGC	1493
Qy	1141	ATTTATGAAATGGTTGTGTCGACGAACACCAATTCAGAAATTAAGAGGAGGTCAGTAA	1200
Db	1494	ATTTATGAAATGGTTGTGTCGACGAACACCAATTCAGAAATTAAGAGGAGGTCAGTAA	1553
Qy	1201	GAGGATCTGAAGCAAGAACTCTGCAAGACGAGGTCAAATTCAGATGATGATTAATCA	1260
Db	1554	GAGGATCTGAAGCAAGAACTCTGCAAGACGAGGTCAAATTCAGATGATGATTAATCA	1613
Qy	1261	GAGGACGAAAGATATTGCGAGGCTCTTCTGCTGAGAAACCAAGAGGAGGCTTAGA	1320
Db	1614	GAGGACGAAAGATATTGCGAGGCTCTTCTGCTGAGAAACCAAGAGGAGGCTTAGA	1673
Qy	1321	AGCAGAGAAAGTCTGATGATCCAGGAAACATCATTTCTTTAAACCGATCAACTTCT	1380
Db	1674	AGCAGAGAAAGTCTGATGATCCAGGAAACATCATTTCTTTAAACCGATCAACTTCT	1733
Qy	1381	CGCTGGAAGCTGCGCTAAATTAAGCCCAATTTGTGCGAGACCCCTTCAAGTGTATGCC	1440
Db	1734	CGCTGGAAGCTGCGCTAAATTAAGCCCAATTTGTGCGAGACCCCTTCAAGTGTATGCC	1793
Qy	1441	AAGACATCGCTGAAATTTGATGATTTCTCTGAGGTTGCGGGGTGGAATTTGATGACAA	1500
Db	1794	AAGACATCGCTGAAATTTGATGATTTCTCTGAGGTTGCGGGGTGGAATTTGATGACAA	1853
Qy	1501	GATAAGCAGTTCTTTCAAAACCTTTGCGACAGGCTGCTTCTATAGCATGGCAGGAGAA	1560
Db	1854	GATAAGCAGTTCTTTCAAAACCTTTGCGACAGGCTGCTTCTATAGCATGGCAGGAGAA	1913
Qy	1561	ATTATAGAAACGGGACTGTTTGAAGAACTGAATGACCCCAACAGACCTTACGGGTTGAG	1620
Db	1914	ATTATAGAAACGGGACTGTTTGAAGAACTGAATGACCCCAACAGACCTTACGGGTTGAG	1973
Qy	1621	GAGGTAATTCATCCAAGTCTGGGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	1659
Db	1974	GAGGTAATTCATCCAAGTCTGGGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	2012

RESULT 7

US-10-217-745-5
; Sequence 5, Application US/10217745
; Publication No. US20030004328A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. US20030004328A1el Human G-Coupled Protein Receptor Kinases ar
; TITLE OF INVENTION: Polynucleotides

```
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/10/217,745
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US/09/802,117
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2249
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-217-745-5

Query Match          99.8%; Score 1655.8; DB 14; Length 2249;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1657; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGTGGACATGGGGCCCTGGACAACTGTATCGCCAAACACCGCCTACCTGACGCCCCGG 60
DB 354 ATGGTGGACATGGGGCCCTGGACAACTGTATCGCCAAACACCGCCTACCTGACGCCCCGG 413

QY 61 AAGCCCTCGGACTGCGACAGCAAGAGCTGCGCGCGCGCGCGCTAGCCTGSCCCTGCC 120
DB 414 AAGCCCTCGGACTGCGACAGCAAGAGCTGCGCGCGCGCGCGCTAGCCTGSCCCTGCC 473

QY 121 GGGCTGACGGCTGCGCGAGCTCGCCAGAAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
DB 474 GGGCTGACGGCTGCGCGAGCTCGCCAGAAAGCTGTCCCTGAACTTCCACAGCCTGTGT 533

QY 181 GAGCAGACGCCCATCGTTCGCGCCTCTTCCGTGACTTCTAGCCACAGTGCACAGTTTC 240
DB 534 GAGCAGACGCCCATCGTTCGCGCCTCTTCCGTGACTTCTAGCCACAGTGCACAGTTTC 593

QY 241 CCGAAGCGGCAACCTTCTAGACAGCTGCGAGAACTGGAGCTGGCGAGAGGAGGCC 300
DB 594 CCGAAGCGGCAACCTTCTAGAGACGTCGCAAGAACTGGAGCTGGCGAGAGGAGGCC 653

QY 301 ACCAAGACAGCGCTGCGAGGGCTGGTGGCCACTTGTGCGAGTGGCCCTGCCCGCGGG 360
DB 654 ACCAAGACAGCGCTGCGAGGGCTGGTGGCCACTTGTGCGAGTGGCCCTGCCCGCGGG 713

QY 361 AACCCGCAACCTTCTCAGCAGCGCGTGGCCACCAAGTGCCAAAGCAGCCACCACTGAG 420
DB 714 AACCCGCAACCTTCTCAGCAGCGCGTGGCCACCAAGTGCCAAAGCAGCCACCACTGAG 773

QY 421 GAAGAGCGAGTGGCTGCACTGACGCTGCGCAGGCTGAGCCATCGCTTCTTGCAGAG 480
DB 774 GAAGAGCGAGTGGCTGCACTGACGCTGCGCAGGCTGAGCCATCGCTTCTTGCAGAG 833

QY 481 CAGCCCTTTAAGGATTTCTGTGACCAAGCGCTTCTACGACAGTCTTCTGAGTGGAACTC 540
DB 834 CAGCCCTTTAAGGATTTCTGTGACCAAGCGCTTCTACGACAGTCTTCTGAGTGGAACTC 893

QY 541 TTCGAGATGCAACCAAGTGTGACAAAGTACTTCACTGAGTTTCAAGTCTCTGGGAAAGGT 600
DB 894 TTCGAGATGCAACCAAGTGTGACAAAGTACTTCACTGAGTTTCAAGTCTCTGGGAAAGGT 953

QY 601 GGTTTTGGGAGGTATGTGCGCTGACAGTGGGAGAGAGTGGCTCTCTTGGGAAAG 660
DB 954 GGTTTTGGGAGGTATGTGCGCTGACAGTGGGAGAGAGTGGGAGAGATGTATGCTGTGAAG 1013

QY 661 AAATGGCAAGAACGGCTGAAGAAAGAGTGGCGAGAGAGTGGCTCTCTTGGGAAAG 720
DB 1014 AAATGGCAAGAACGGCTGAAGAAAGAGTGGCGAGAGAGTGGCTCTCTTGGGAAAG 1073

QY 721 GAAATCTTGGAGAGGTGACAGCCCTTTCATGTCTCTGCGCTATGCTTTGAGAGC 780
DB 1074 GAAATCTTGGAGAGGTGACAGCCCTTTCATGTCTCTGCGCTATGCTTTGAGAGC 1133

QY 781 AAGACCCATCTCTGCTTGTGATGAGCCTGTATGAGTGGGAGAGCTCAAGTTCACATC 840
DB 1134 AAGACCCATCTCTGCTTGTGATGAGCCTGTATGAGTGGGAGAGCTCAAGTTCACATC 1193
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QY 841 TACAACGTGGCAGCGTGGCTGGACATGAGCGGGTGATCTTTTACTCGSCCCAGATA 900
DB 1194 TACAACGTGGCAGCGTGGCTGGACATGAGCGGGTGATCTTTTACTCGSCCCAGATA 1253

QY 901 GCCTGTGGATGCTGCACCTCCATCAACTCGGCACTCGTCTATCGGGACATGAAGCCTGAG 960
DB 1254 GCCTGTGGATGCTGCACCTCCATCAACTCGGCACTCGTCTATCGGGACATGAAGCCTGAG 1313

QY 961 AATGTGCTTCTGGATGACCTCGGCAACTGCAAGTTATCTGACCTGGGGCTGGCGTGGAG 1020
DB 1314 AATGTGCTTCTGGATGACCTCGGCAACTGCAAGTTATCTGACCTGGGGCTGGCGTGGAG 1373

QY 1021 ATGAAGGGTGGCAAGCCCATCACAGAGGCTCGAACTAATGGTTACATGGCTCCTGAG 1080
DB 1374 ATGAAGGGTGGCAAGCCCATCACAGAGGCTCGAACTAATGGTTACATGGCTCCTGAG 1433

QY 1081 ATCTTAATGAAAAAGGTAAGTTATTCCTATCTCTGGAAGTGGCTTTGCCATGGGATGACG 1140
DB 1434 ATCTTAATGAAAAAGGTAAGTTATTCCTATCTCTGGAAGTGGCTTTGCCATGGGATGACG 1493

QY 1141 ATTTATGAATGGTGTCTGGAGCAACACCATTCAGAGTTTCAAGATTCAAGAGAAAGGTCAGTAAA 1200
DB 1494 ATTTATGAATGGTGTCTGGAGCAACACCATTCAGAGTTTCAAGATTCAAGAGAAAGGTCAGTAAA 1553

QY 1201 GAGGATCTGAAGCAAGAACTCTCAAGACGAGGTCAAATTCAGACATGATACTTCAACA 1260
DB 1554 GAGGATCTGAAGCAAGAACTCTCAAGACGAGGTCAAATTCAGACATGATACTTCAACA 1613

QY 1261 GAGGAACCAAGATATTTGCAAGCTCTTCTTGGCTTAAGAAACAGACCAACGCTTAGGA 1320
DB 1614 GAGGAACCAAGATATTTGCAAGCTCTTCTTGGCTTAAGAAACAGACCAACGCTTAGGA 1673

QY 1321 AGCAGAGAAAGTCTGATGATCCAGGAAACATCATTTCTTTAAACGATCAACTTTCCT 1380
DB 1674 AGCAGAGAAAGTCTGATGATCCAGGAAACATCATTTCTTTAAACGATCAACTTTCCT 1733

QY 1381 CGCTTGAAGTGGCCCTAAATTTGAACCCCTTCTTGGCCAGACCTTCAAGTGGTTTATGCC 1440
DB 1734 CGCTTGAAGTGGCCCTAAATTTGAACCCCTTCTTGGCCAGACCTTCAAGTGGTTTATGCC 1793

QY 1441 AAAGACATGCTGAAATGATGATTTCTGAGGTTTCGGGGGGTGGAAATTTGATGACAAA 1500
DB 1794 AAAGACATGCTGAAATGATGATTTCTGAGGTTTCGGGGGGTGGAAATTTGATGACAAA 1853

QY 1501 GATAAGCAGTTCTTCAAAACTTTTGCACAGGCTGCTTCTCTATAGCATGCGCAGAGAAA 1560
DB 1854 GATAAGCAGTTCTTCAAAACTTTTGCACAGGCTGCTTCTCTATAGCATGCGCAGAGAAA 1913

QY 1561 ATTATAGAAACGGGACTGTTTGAAGAACTGAATGACCCCAACAGACCTTACGGGTGTGAG 1620
DB 1914 ATTATAGAAACGGGACTGTTTGAAGAACTGAATGACCCCAACAGACCTTACGGGTGTGAG 1973

QY 1621 GAGGTAATTCATCAAGTCTGGCGTGTGTTGTTATG 1659
DB 1974 GAGGTAATTCATCAAGTCTGGCGTGTGTTGTTATG 2012
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RESULT 8

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US-09-802-117-1
; Sequence 1, Application US/09802117
; Publication No. US20020042503A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6444561 Human G-Coupled Protein Receptor Kinases and Polym
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/09/802,117
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/188,449
; PRIOR FILING DATE: 2000-03-10
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; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-802-117-1

Query Match 99.8%; Score 1655.4; DB 9; Length 1662;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1656; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGTGGACATGGGGCCCTGACAACTGATCGCAACACCGCTACTGACGAGCCGG 60
DB 1 ATGTGGACATGGGGCCCTGGAYAACTGATCGCAACACCGCTACTGACGAGCCGG 60

QY 61 AAGCCCTCGGACTGCGACAGCAAGAGCTGCAAGCGCGCGGTAGCTGSCCTGCCC 120
DB 61 AAGCCCTCGGACTGCGACAGCAAGAGCTGCAAGCGCGCGGTAGCTGSCCTGCCC 120

QY 121 GGGCTGCAAGGCTGCGCGAGCTCGCGCCAGAAAGCTGTCCCTGAACTTCCACAGCCTGTG 180
DB 121 GGGCTGCAAGGCTGCGCGAGCTCGCGCCAGAAAGCTGTCCCTGAACTTCCACAGCCTGTG 180

QY 181 GAGCAGAGCCCATCGGTGCGCGCTCTTCCGTGACTTCTTAGCCACAGTGCACAGTTC 240
DB 181 GAGCAGAGCCCATCGGTGCGCGCTCTTCCGTGACTTCTTAGCCACAGTGCACAGTTC 240

QY 241 CGCAGGCGGCAACCTTCTAGAGACGTGCAAGAACTGGAGCTGGCGAGGAGGCC 300
DB 241 CGCAGGCGGCAACCTTCTAGAGACGTGCAAGAACTGGAGCTGGCGAGGAGGCC 300

QY 301 ACCAAGACAGCGCTGCGAGGCTGTGGCCACTTGTGAGTGGCCCTCCCGCGGG 360
DB 301 ACCAAGACAGCGCTGCGAGGCTGTGGCCACTTGTGAGTGGCCCTCCCGCGGG 360

QY 361 AACCGCAACCTTCTCAGCAGCGCGTGGCCACCAAGTGGCAAGCAGCAGCCACTGAG 420
DB 361 AACCGCAACCTTCTCAGCAGCGCGTGGCCACCAAGTGGCAAGCAGCAGCCACTGAG 420

QY 421 GAAGCCGAGTGGCTGCAAGTGGCTGCGCAGGCTGAGCCATGGCTTCTTGAAG 480
DB 421 GAAGCCGAGTGGCTGCAAGTGGCTGCGCAGGCTGAGCCATGGCTTCTTGAAG 480

QY 481 CAGCCCTTTAAGATTTCTGACCAAGCGCTTCTAGCAAGTCTTCTGAGTGGAACTC 540
DB 481 CAGCCCTTTAAGATTTCTGACCAAGCGCTTCTAGCAAGTCTTCTGAGTGGAACTC 540

QY 541 TTCGAGATGCAACCAAGTGTGACCAAGTACTTCACTGAGTTCAGAGTCTGGGAAAGT 600
DB 541 TTCGAGATGCAACCAAGTGTGACCAAGTACTTCACTGAGTTCAGAGTCTGGGAAAGT 600

QY 601 GGTGGGAGGTATGCGCTGAGTGAAGAACTGGGAACTGATGATGCTGTAAG 660
DB 601 GGTGGGAGGTATGCGCTGAGTGAAGAACTGGGAACTGATGATGCTGTAAG 660

QY 661 AAATGGAACAAGCGCTGAAGAAAGTGGCAAGTGGCTCTCTTGGAAAG 720
DB 661 AAATGGAACAAGCGCTGAAGAAAGTGGCAAGTGGCTCTCTTGGAAAG 720

QY 721 GAAATCTTGGAGAGGTGACAGCCCTTTCAATGTCTCTGCGCTATGCTTGGAGC 780
DB 721 GAAATCTTGGAGAGGTGACAGCCCTTTCAATGTCTCTGCGCTATGCTTGGAGC 780

QY 781 AAGACCCATCTCTGCTTGTATGAGCTGATGAGTGGGGAGACCTCAAGTTCACATC 840
DB 781 AAGACCCATCTCTGCTTGTATGAGCTGATGAGTGGGGAGACCTCAAGTTCACATC 840

QY 841 TACAACGTGGGACCGCTGGACATGACCGGTGATCTTTTACTCGGCCAGATA 900
DB 841 TACAACGTGGGACCGCTGGACATGACCGGTGATCTTTTACTCGGCCAGATA 900

QY 901 GCCTGTGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

RESULT 9

US-10-217-745-1
; Sequence 1, Application US/10217745
; Publication No. US20030004328A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. US20030004328A1el Human G-Coupled Protein Receptor Kinases an
; TITLE OF INVENTION: Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/10/217,745
; PRIORITY FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US/09/802,117
; PRIORITY FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1662
; TYPE: DNA

DB 901 GCCTGTGGATGCTGCACCTCATGAACCTCGCATCGTCTATCGGGACATGAAGCCTGAG 960

QY 961 AATGTGCTTCTGGATGACCTCGGCAACTGCAAGTCTATCTGACCTGGGGCTGCGCGTGGAG 1020

DB 961 AATGTGCTTCTGGATGACCTCGGCAACTGCAAGTCTATCTGACCTGGGGCTGCGCGTGGAG 1020

QY 1021 ATGAAGGTGGCAAGCCCATCACCAGAGGGCTGGAACAATGGTTACATGGCTCTGAG 1080

DB 1021 ATGAAGGTGGCAAGCCCATCACCAGAGGGCTGGAACAATGGTTACATGGCTCTGAG 1080

QY 1081 ATCTTAATGGAAGGTAAGTATTCTCTATCTCTGGAAGTGGTTGGCCATGGGATGCAGC 1140

DB 1081 ATCTTAATGGAAGGTAAGTATTCTCTATCTCTGGAAGTGGTTGGCCATGGGATGCAGC 1140

QY 1141 ATTTATGAAATGTTGCTGGAAGCAACCACTTCAAGATTTACAAGAAAGGTCAGTAAA 1200

DB 1141 ATTTATGAAATGTTGCTGGAAGCAACCACTTCAAGATTTACAAGAAAGGTCAGTAAA 1200

QY 1201 GAGGATCTGAAGCAAGAACTCTGCAAGCAGAGTCAAAATCCAGCATGATTAATCTTACA 1260

DB 1201 GAGGATCTGAAGCAAGAACTCTGCAAGCAGAGTCAAAATCCAGCATGATTAATCTTACA 1260

QY 1261 GAGGAGCAAAAGATATTTGCAAGGCTCTTCTGCTAGAAACCAAGCAAGCCTTAGGA 1320

DB 1261 GAGGAGCAAAAGATATTTGCAAGGCTCTTCTGCTAGAAACCAAGCAAGCCTTAGGA 1320

QY 1321 AGCAGAGAAAGTCTGATGATGATCCCAAGGAAACATCATTTCTTTAAACGATCAACTTCT 1380

DB 1321 AGCAGAGAAAGTCTGATGATGATCCCAAGGAAACATCATTTCTTTAAACGATCAACTTCT 1380

QY 1381 CGCTGGAAGCTGGCTTAATTAAGCCCAATTTGTCAGAGCCCTTCACTGAGTGGTTATGCC 1440

DB 1381 CGCTGGAAGCTGGCTTAATTAAGCCCAATTTGTCAGAGCCCTTCACTGAGTGGTTATGCC 1440

QY 1441 AAAGCATCGCTGAAATGATGATTTCTGAGGTTGCGGGGGTGGAAATTTGATGACAAA 1500

DB 1441 AAAGCATCGCTGAAATGATGATTTCTGAGGTTGCGGGGGTGGAAATTTGATGACAAA 1500

QY 1501 GATAGCAGTCTTCAAAACCTTTGCGACAGTGTCTTCTATAGCATGGCAGGAAGA 1560

DB 1501 GATAGCAGTCTTCAAAACCTTTGCGACAGTGTCTTCTATAGCATGGCAGGAAGA 1560

QY 1561 ATTATAGAAACGGGACTGTTTGAAGAACTGAATGACCCCAAGACCTACCGGTTGTGAG 1620

DB 1561 ATTATAGAAACGGGACTGTTTGAAGAACTGAATGACCCCAAGACCTACCGGTTGTGAG 1620

QY 1621 GAGGTAATTCATCCAGTCTGGCGTGTGTTTATTG 1659

DB 1621 GAGGTAATTCATCCAGTCTGGCGTGTGTTTATTG 1659

ORGANISM: homo sapiens
US-10-217-745-1

Query Match 99.8%; Score 1655.4; DB 14; Length 1662;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1656; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY	1	ATGGTGGACATGGGGCCCTGGACAACTGATCGCAACACCGCCTACTGCGAGCCCGG	60
DB	1	ATGGTGGACATGGGGCCCTGGAYAACCTGATCGCAACACCGCCTACTGCGAGCCCGG	60
QY	61	AAGCCCTCGGACTGGACAGCAAAAGAGTGCAGCGCGCGCGTAGCCTGCCCC	120
DB	61	AAGCCCTCGGACTGGACAGCAAAAGAGTGCAGCGCGCGCGTAGCCTGCCCC	120
QY	121	GGGCTCGAGGCTGGCGGAGCTCGCCAGAGCTGCTCCCTGAACTTCCACAGCCCTGT	180
DB	121	GGGCTCGAGGCTGGCGGAGCTCGCCAGAGCTGCTCCCTGAACTTCCACAGCCCTGT	180
QY	181	GAGCAGCAGCCCATCGCTCGCGCCTCTTCCGTGACTTCTAGCCACAGTGCACAGTTC	240
DB	181	GAGCAGCAGCCCATCGCTCGCGCCTCTTCCGTGACTTCTAGCCACAGTGCACAGTTC	240
QY	241	CGCAAGCGGCAACCTTCTTAGAGACGTGCAGAACTGGAGCTGGCCGAGGAGGCC	300
DB	241	CGCAAGCGGCAACCTTCTTAGAGACGTGCAGAACTGGAGCTGGCCGAGGAGGCC	300
QY	301	ACCAAGACAGCGCGCTGAGGGGCTGGTGGCCACTTGTGGAGTGGCCCCCGGG	360
DB	301	ACCAAGACAGCGCGCTGAGGGGCTGGTGGCCACTTGTGGAGTGGCCCCCGGG	360
QY	361	AACCCGCAACCTTCTCAGCAGCGCGCTGGCCACCAAGTGCAGCAGCCACCACTGAG	420
DB	361	AACCCGCAACCTTCTCAGCAGCGCGCTGGCCACCAAGTGCAGCAGCCACCACTGAG	420
QY	421	GAAGAGCGAGTGGCTGCAGTGCAGTGCAGAAAGTGCAGGCTGGCTTTCTTGAAGAG	480
DB	421	GAAGAGCGAGTGGCTGCAGTGCAGTGCAGAAAGTGCAGGCTGGCTTTCTTGAAGAG	480
QY	481	CAGCCCTTTAAGGATTTGTGACACAGCGCTTCTACGACAGTTTCTCAGTGGAACTC	540
DB	481	CAGCCCTTTAAGGATTTGTGACACAGCGCTTCTACGACAGTTTCTCAGTGGAACTC	540
QY	541	TTGAGATGCAACCAAGTGTGCAGCAAGTACTTCACTGAGTGCAGAGTGCCTGGGAAAG	600
DB	541	TTGAGATGCAACCAAGTGTGCAGCAAGTACTTCACTGAGTGCAGAGTGCCTGGGAAAG	600
QY	601	GGTTTGGGAGGTATGTGCGCTCAGGTGAAACACACTGGGAAGATGTATGCTGTAAAG	660
DB	601	GGTTTGGGAGGTATGTGCGCTCAGGTGAAACACACTGGGAAGATGTATGCTGTAAAG	660
QY	661	AAACTGGCAAGAACGGCTGAAGAAAGTGGGAGAGATGGCTCTCTTGGAAAG	720
DB	661	AAACTGGCAAGAACGGCTGAAGAAAGTGGGAGAGATGGCTCTCTTGGAAAG	720
QY	721	GAATCTTTGGAAGGTGCAGAGCCCTTTCACTGCTCTGGCTATGCTGGAGC	780
DB	721	GAATCTTTGGAAGGTGCAGAGCCCTTTCACTGCTCTGGCTATGCTGGAGC	780
QY	781	AAGACCATCTGCTGCTGTATGAGCTGATGAATGGGGAGACCTCAAGTTCACATC	840
DB	781	AAGACCATCTGCTGCTGTATGAGCTGATGAATGGGGAGACCTCAAGTTCACATC	840
QY	841	TACACGTGGGACGCGTGGCTGACATGAGCGGGTGATCTTTTACTCGGCCAGATA	900
DB	841	TACACGTGGGACGCGTGGCTGACATGAGCGGGTGATCTTTTACTCGGCCAGATA	900
QY	901	GCCTGTGGATGCTGACCTCCATCACTCGCATCGTCTATCGGACATGAAGCTGAG	960
DB	901	GCCTGTGGATGCTGACCTCCATCACTCGCATCGTCTATCGGACATGAAGCTGAG	960
QY	961	AATGTGCTTCTGGATGACTCGGCAACTGACAGTTATCTGACCTGGGCTGGCGTGGAG	1020
DB			

DB	961	AATGTGCTTCTGGATGACTCGGCAACTGACAGTTATCTGACCTGGGCTGGCGTGGAG	1020
QY	1021	ATGAGGGTGGCAAGCCCATCACCAGAGGCTGGACCAATGTTACATCGCTCCTGAG	1080
DB	1021	ATGAGGGTGGCAAGCCCATCACCAGAGGCTGGACCAATGTTACATCGCTCCTGAG	1080
QY	1081	ATCCTAATGGAAGAGTAAAGTTATTCCTATCCTGTGACTGTTTGCATGGGATGACG	1140
DB	1081	ATCCTAATGGAAGAGTAAAGTTATTCCTATCCTGTGACTGTTTGCATGGGATGACG	1140
QY	1141	ATTTATGAATGTTGCTGGACGAACCAATTCATAAGATTAACAAGGAAAGGTCAATAA	1200
DB	1141	ATTTATGAATGTTGCTGGACGAACCAATTCATAAGATTAACAAGGAAAGGTCAATAA	1200
QY	1201	GAGGATCTGAAGCAAGAACTCTCAAGACAGGTCAAAATCCAGCATGATACTTACA	1260
DB	1201	GAGGATCTGAAGCAAGAACTCTCAAGACAGGTCAAAATCCAGCATGATACTTACA	1260
QY	1261	GAGGAAGCAAAAGATATTTGACGGCTCTTCTTGGCTAAGAAACCAAGCAACGCTTAGGA	1320
DB	1261	GAGGAAGCAAAAGATATTTGACGGCTCTTCTTGGCTAAGAAACCAAGCAACGCTTAGGA	1320
QY	1321	AGCAGAGAAAGTCTGATGATCCAGGAAACATCATTTCTTTAAAAACATCACTTCT	1380
DB	1321	AGCAGAGAAAGTCTGATGATCCAGGAAACATCATTTCTTTAAAAACATCACTTCT	1380
QY	1381	CGCTGGAAGCTGCCTAAATTTGAACCCCTTTTGTCCAGACCCCTTCACTGTTTATGCC	1440
DB	1381	CGCTGGAAGCTGCCTAAATTTGAACCCCTTTTGTCCAGACCCCTTCACTGTTTATGCC	1440
QY	1441	AAAGACATCGCTGAAATTTGATGATTTCTGAGGTTGCGGGGTGGATTTGATGACAAA	1500
DB	1441	AAAGACATCGCTGAAATTTGATGATTTCTGAGGTTGCGGGGTGGATTTGATGACAAA	1500
QY	1501	GATAAGCAGTTCTTCAAAAACCTTTGCGACAGTCTGTTCTATAGCATGCGAGAGAA	1560
DB	1501	GATAAGCAGTTCTTCAAAAACCTTTGCGACAGTCTGTTCTATAGCATGCGAGAGAA	1560
QY	1561	ATTATAGAAACGGGACTGTTTGAAGAACTGAATGACCCCAACAGACCTTACGGGTTGAG	1620
DB	1561	ATTATAGAAACGGGACTGTTTGAAGAACTGAATGACCCCAACAGACCTTACGGGTTGAG	1620
QY	1621	GAGGTAATTCATCAAGTCTGCGGTGTTGTTTATG 1659	
DB	1621	GAGGTAATTCATCAAGTCTGCGGTGTTGTTTATG 1659	

RESULT 10

US-09-964-469-1
; Sequence 1, Application US/09964469
; Patent No. US20020034803A1

GENERAL INFORMATION:

APPLICANT: GUEGLER, Karl et al

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

FILE REFERENCE: CL000636DIV

CURRENT APPLICATION NUMBER: US/09/964,469

CURRENT FILING DATE: 2001-09-28

PRIOR APPLICATION NUMBER: 60/208,331

PRIOR FILING DATE: 2000-06-01

PRIOR APPLICATION NUMBER: 09/738,894

PRIOR FILING DATE: 2000-12-18

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1

LENGTH: 1662

TYPE: DNA

ORGANISM: Human

US-09-964-469-1

Query Match 99.7%; Score 1654.2; DB 9; Length 1662;
Best Local Similarity 99.8%; Pred. No. 0;

Matches 1656; Conservative 0; Mismatches 3; Indels 0; Gaps 0;			
Qy	1	ATGTGGGATGGGGCCCTGGCAACCTGATCGCAACACCGCCTACCTGCGAGCCCGG	60
Db	1	ATGTGGGATGGGGCCCTGGCAACCTGATCGCAACACCGCCTACCTGCGAGCCCGG	60
Qy	61	AAGCCCTCGGACTGGACAGCAAGAGCTGCAAGCGCGCGGCTAGCCTGCGCCTGCC	120
Db	61	AAGCCCTCGGACTGGACAGCAAGAGCTGCAAGCGCGCGGCTAGCCTGCGCCTGCC	120
Qy	121	GGGCTGCGAGGGCTGGCGGAGCTCGCGAGAGCTGCTCCTGAACTTCCACAGCCTGTGT	180
Db	121	GGGCTGCGAGGGCTGGCGGAGCTCGCGAGAGCTGCTCCTGAACTTCCACAGCCTGTGT	180
Qy	181	GAGCAGAGCCCATCGGTGCGCCCTCTTCCGTGACTTCTTAGCCACAGTGCACAGTTC	240
Db	181	GAGCAGAGCCCATCGGTGCGCCCTCTTCCGTGACTTCTTAGCCACAGTGCACAGTTC	240
Qy	241	CGAAGGGGGAACTTCTTAGAGAGCTGCGAGAACTGGGAGCTGGCGAGGAGGAGCC	300
Db	241	CGAAGGGGGAACTTCTTAGAGAGCTGCGAGAACTGGGAGCTGGCGAGGAGGAGCC	300
Qy	301	ACCAAGACAGCGCGCTGCGAGGGCTGTGGCCACTTGTGCGAGTGCCTGCCCGGGG	360
Db	301	ACCAAGACAGCGCGCTGCGAGGGCTGTGGCCACTTGTGCGAGTGCCTGCCCGGGG	360
Qy	361	AACCCGCAACCTTCTCAGCGAGCGCTGGCCACCAAGTGCCAGAGCCACCACTGAG	420
Db	361	AACCCGCAACCTTCTCAGCGAGCGCTGGCCACCAAGTGCCAGAGCCACCACTGAG	420
Qy	421	GAAGAGCGAGTGGCTGCACTGAGCTGGCGAAGCTGAGGCGCATGGCTTTCTTGAAG	480
Db	421	GAAGAGCGAGTGGCTGCACTGAGCTGGCGAAGCTGAGGCGCATGGCTTTCTTGAAG	480
Qy	481	CAGCCCTTTAGGATTTCTGACAGCGCTTCTAGGACAGTTCCTGAGTGGAACTC	540
Db	481	CAGCCCTTTAGGATTTCTGACAGCGCTTCTAGGACAGTTCCTGAGTGGAACTC	540
Qy	541	TTGAGATGCAACCACTGTGAGCAAGTACTTCACTGAGTTCAGAGTGTGGGAAAGT	600
Db	541	TTGAGATGCAACCACTGTGAGCAAGTACTTCACTGAGTTCAGAGTGTGGGAAAGT	600
Qy	601	GTTTGGGAGGATATGTCCTCAGGTGAAACACCTGGGAAAGATGATGCTGTGAAG	660
Db	601	GTTTGGGAGGATATGTCCTCAGGTGAAACACCTGGGAAAGATGATGCTGTGAAG	660
Qy	661	AACTGGACAGAGCGCTGAGAGAAAGTGGCGAGAGATGGCTCTTTGGAAG	720
Db	661	AACTGGACAGAGCGCTGAGAGAAAGTGGCGAGAGATGGCTCTTTGGAAG	720
Qy	721	GAAATCTTGGAGAGGTGAGAGCGCTTTCATGTCTCTGCGCTATGCTTTCAGAGC	780
Db	721	GAAATCTTGGAGAGGTGAGAGCGCTTTCATGTCTCTGCGCTATGCTTTCAGAGC	780
Qy	781	AAGACCCATCTGCTTGTATGAGCTGATGAATGGGGAGAGCTCAAGTTCACATC	840
Db	781	AAGACCCATCTGCTTGTATGAGCTGATGAATGGGGAGAGCTCAAGTTCACATC	840
Qy	841	TACAACTGGGACCGGCTGAGACATGAGCCGGTGTCTTTTACTCGGCCCAGATA	900
Db	841	TACAACTGGGACCGGCTGAGACATGAGCCGGTGTCTTTTACTCGGCCCAGATA	900
Qy	901	GCCTGTGGATGCTGCACCTCCATCACTCGGCATGCTCTATCGGGAGATGAAGCTGAG	960
Db	901	GCCTGTGGATGCTGCACCTCCATCACTCGGCATGCTCTATCGGGAGATGAAGCTGAG	960
Qy	961	AATGTGCTTCTGGATGACCTCGGCAACTGCAAGTTATCTGACCTGGGGCTGGCGTGAG	1020
Db	961	AATGTGCTTCTGGATGACCTCGGCAACTGCAAGTTATCTGACCTGGGGCTGGCGTGAG	1020
Qy	1021	ATGAAGGGTGGCAAGCCATCAACCGAGGGCTGGAACCAATGGTTACAGGCTCCTGAG	1080
Db	1021	ATGAAGGGTGGCAAGCCATCAACCGAGGGCTGGAACCAATGGTTACAGGCTCCTGAG	1080

Qy	1081	ATCCTAATGGAAGGTAAGTATTCTCTATCTCTGGAAGTCTGTTGCCATGGGATGCGAGC	1140
Db	1081	ATCCTAATGGAAGGTAAGTATTCTCTATCTCTGGAAGTCTGTTGCCATGGGATGCGAGC	1140
Qy	1141	ATTTATGAATGGTGTCTGGAGACACCATTTCAAGATTTCAAGAAAGGTCTAGTAAA	1200
Db	1141	ATTTATGAATGGTGTCTGGAGACACCATTTCAAGATTTCAAGAAAGGTCTAGTAAA	1200
Qy	1201	GAGGATCTGAAGCAAGAACTCTGCAAGCAGAGTCAAAATTCAGCATGATTAACATTACA	1260
Db	1201	GAGGATCTGAAGCAAGAACTCTGCAAGCAGAGTCAAAATTCAGCATGATTAACATTACA	1260
Qy	1261	GAGGAAGCAAAAGATATTGCGAGGCTCTTCTTGGCTAAGAAACCAAGCAAGCTTAGGA	1320
Db	1261	GAGGAAGCAAAAGATATTGCGAGGCTCTTCTTGGCTAAGAAACCAAGCAAGCTTAGGA	1320
Qy	1321	AGCAGAGAAAGTCTGATGATCCAGGAAACATCATTTCTTTAAACCATCACTTCTCT	1380
Db	1321	AGCAGAGAAAGTCTGATGATCCAGGAAACATCATTTCTTTAAACCATCACTTCTCT	1380
Qy	1381	CGCTGGAAGCTGGCTAAATTTGAACCCCATTTGTGCCAGACCCCTTCAGTGGTTATGCC	1440
Db	1381	CGCTGGAAGCTGGCTAAATTTGAACCCCATTTGTGCCAGACCCCTTCAGTGGTTATGCC	1440
Qy	1441	AAAGACATCGCTGAAATTTGATGATTTCTCTGAGGTTGCGGGGGTGGAAATTTGATGACAAA	1500
Db	1441	AAAGACATCGCTGAAATTTGATGATTTCTCTGAGGTTGCGGGGGTGGAAATTTGATGACAAA	1500
Qy	1501	GATAGAGAGTCTTCAAAAACCTTTGCGAGAGTGTCTCTATAGCATGGCAGGAAGAA	1560
Db	1501	GATAGAGAGTCTTCAAAAACCTTTGCGAGAGTGTCTCTCTATAGCATGGCAGGAAGAA	1560
Qy	1561	ATTATAGAAACGGAGCTGTTTGAAGAACTGAATGACCCCAACAGACCTACGGTTGTGAG	1620
Db	1561	ATTATAGAAACGGAGCTGTTTGAAGAACTGAATGACCCCAACAGACCTACGGTTGTGAG	1620
Qy	1621	GAGGTAATTCATCCAACTCTGGCGTGTGTTTATTG 1659	
Db	1621	GAGGTAATTCATCCAACTCTGGCGTGTGTTTATTG 1659	

RESULT 11
US-10-425-962-1
; Sequence 1, Application US/10425962
; Publication No. US20030180786A1
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CLO00636DIV2
; CURRENT APPLICATION NUMBER: US/10425,962
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 09/964,469
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 09/738,894
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/208,331
; PRIOR FILING DATE: 2000-06-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-425-962-1

Query Match	99.7%	Score 1654.2;	DB 16;	Length 1662;
Best Local Similarity	99.8%	Pred. No. 0;		
Matches 1656;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
Qy	1	ATGTGGACATGGGGCCCTGGCAACCTGATCGCAACACCGCCTACCTGCGAGCCCGG	60	

Db 1 ATGTGGACATGGGGGCTCGACAACTGATCGCAACACCGCTACCTCGAGCCCGG 60
Qy 61 AAGCCTCGGACTCGGACAGCAAGAGCTGCAGCGCGCGCGGTAGCCTGCGCCCTGCC 120
Db 61 AAGCCTCGGACTCGGACAGCAAGAGCTGCAGCGCGCGCGGTAGCCTGCGCCCTGCC 120
Qy 121 GGGCTGACAGGGTGGCGGAGCTCGCGCAGAGCTGTCCCTGAATTCACAGCCTGTGT 180
Db 121 GGGCTGACAGGGTGGCGGAGCTCGCGCAGAGCTGTCCCTGAATTCACAGCCTGTGT 180
Qy 181 GAGCAGAGCCCATCGGTGCGGCTCTTCGTGACTTCCTAGCACAAGTGGCCGACGTTT 240
Db 181 GAGCAGAGCCCATCGGTGCGGCTCTTCGTGACTTCCTAGCACAAGTGGCCGACGTTT 240
Qy 241 CGCAGGCGGCAACCTTCTGAGGACGTGCAGAACTGGGAGCTGGCGAGGAGGAGCC 300
Db 241 CGCAGGCGGCAACCTTCTGAGGACGTGCAGAACTGGGAGCTGGCGAGGAGGAGCC 300
Qy 301 ACCAAGACAGCGGCTGCAGGGGCTGTGGCCACTTGTGCGAGTGGCCCTGCCCCGGG 360
Db 301 ACCAAGACAGCGGCTGCAGGGGCTGTGGCCACTTGTGCGAGTGGCCCTGCCCCGGG 360
Qy 361 AACCCGCAACCTTCTGAGCAGGCGGTGGCCACCAAGTGCACAGCAGCCACTGAG 420
Db 361 AACCCGCAACCTTCTGAGCAGGCGGTGGCCACCAAGTGCACAGCAGCCACTGAG 420
Qy 421 GAAGAGCAGTGGCTGCAGTACGCTGCGCAAGGCTGAGGCGCATGGCTTCTTGAAG 480
Db 421 GAAGAGCAGTGGCTGCAGTACGCTGCGCAAGGCTGAGGCGCATGGCTTCTTGAAG 480
Qy 481 CAGCCCTTTAAGATTTCTGACACAGCGCTTCTACGACAGTGTCTGAGTGGAACTC 540
Db 481 CAGCCCTTTAAGATTTCTGACACAGCGCTTCTACGACAGTGTCTGAGTGGAACTC 540
Qy 541 TTCGAGATGCAACAGTGTGACAGAACTTCTACAGTTCAGAGTCTGCGGAAAGGT 600
Db 541 TTCGAGATGCAACAGTGTGACAGAACTTCTACAGTTCAGAGTCTGCGGAAAGGT 600
Qy 601 GGTGTTGGGAGTGTGCTGCTGATGAGCTGATGAAACACTGGGAAGATGTATGCTGTAAG 660
Db 601 GGTGTTGGGAGTGTGCTGCTGATGAGCTGATGAAACACTGGGAAGATGTATGCTGTAAG 660
Qy 661 AAATGGAACAAGCGGCTGAAGAAAGTGGCGAGAGATGGCTCTCTTGGAAAG 720
Db 661 AAATGGAACAAGCGGCTGAAGAAAGTGGCGAGAGATGGCTCTCTTGGAAAG 720
Qy 721 GAAATCTTGGAGAGGTGAGAGCCCTTCTATGCTCTGCGCTATGCTTGGAGGC 780
Db 721 GAAATCTTGGAGAGGTGAGAGCCCTTCTATGCTCTGCGCTATGCTTGGAGGC 780
Qy 781 AAGACCCATCTGCTGCTGATGAGCTGATGAAATGGGGAGACCTCAAGTTCCACATC 840
Db 781 AAGACCCATCTGCTGCTGATGAGCTGATGAAATGGGGAGACCTCAAGTTCCACATC 840
Qy 841 TACAACGTGGGACGCGTGGCTGGACATGAGCGGGTGAATTTTATCTGCGCCAGATA 900
Db 841 TACAACGTGGGACGCGTGGCTGGACATGAGCGGGTGAATTTTATCTGCGCCAGATA 900
Qy 901 GCCTGGGATGCTGACCTCATGACCTCGGATCGTCTATCGGACATGAGGCTGAG 960
Db 901 GCCTGGGATGCTGACCTCATGACCTCGGATCGTCTATCGGACATGAGGCTGAG 960
Qy 961 AATGCTTCTGATGATCTCGGCAACTGACGTTATCTGACCTGGGCTGGCGTGGAG 1020
Db 961 AATGCTTCTGATGATCTCGGCAACTGACGTTATCTGACCTGGGCTGGCGTGGAG 1020
Qy 1021 ATGAAGGTGGCAAGCCATCACAGAGGGTGGAAACCAATGGTTACATGGCTCTGAG 1080
Db 1021 ATGAAGGTGGCAAGCCATCACAGAGGGTGGAAACCAATGGTTACATGGCTCTGAG 1080
Qy 1081 ATCTAATGGAAGGTAAGTTATTCCTATCTGTGAACTGTTTGGCATGGATGACG 1140

Db 1081 ATCTAATGGAAGGTAAGTTATTCCTATCTGTGAACTGTTTGGCATGGATGACG 1140
Qy 1141 ATTTATGAATGGTTGCTGGAGCAACCAATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200
Db 1141 ATTTATGAATGGTTGCTGGAGCAACCAATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200
Qy 1201 GAGGATCTGAAGCAAGAACTCTGCAAGACGAGGTCAAATTCAGCATGATACTTCACA 1260
Db 1201 GAGGATCTGAAGCAAGAACTCTGCAAGACGAGGTCAAATTCAGCATGATACTTCACA 1260
Qy 1261 GAGGAGCAAGAAATATTGACAGCTCTTCTGGCTAAGAAACAGACCAAGCTTAGGA 1320
Db 1261 GAGGAGCAAGAAATATTGACAGCTCTTCTGGCTAAGAAACAGACCAAGCTTAGGA 1320
Qy 1321 AGCAGAGAAAGTCTGATGATCCAGGAAACATCATTTCTTTAAACGATCAACTTCT 1380
Db 1321 AGCAGAGAAAGTCTGATGATCCAGGAAACATCATTTCTTTAAACGATCAACTTCT 1380
Qy 1381 CGCTGAGAGTGGCTTAATTTGAACCCCAATTTGTCAGACCCCTTCAGTGGTTATGCC 1440
Db 1381 CGCTGAGAGTGGCTTAATTTGAACCCCAATTTGTCAGACCCCTTCAGTGGTTATGCC 1440
Qy 1441 AAAGACATCGCTGAAATTTGATGATTTCTCTGAGGTTGCGGGGTGGAATTTGATGACAAA 1500
Db 1441 AAAGACATCGCTGAAATTTGATGATTTCTCTGAGGTTGCGGGGTGGAATTTGATGACAAA 1500
Qy 1501 GATAAGCAGTTCTTTCAAAAACCTTTGCGACAGGTGCTGTTCTATAGCATGCGAGAGAA 1560
Db 1501 GATAAGCAGTTCTTTCAAAAACCTTTGCGACAGGTGCTGTTCTATAGCATGCGAGAGAA 1560
Qy 1561 ATTATAGAAACGGAGCTGTTGAGAACTGAATGACCCCAACAGACCTTACGGTGTGAG 1620
Db 1561 ATTATAGAAACGGAGCTGTTGAGAACTGAATGACCCCAACAGACCTTACGGTGTGAG 1620
Qy 1621 GAGGTAATTCATCAAGTCTGGGCTGTTGTTATTG 1659
Db 1621 GAGGTAATTCATCAAGTCTGGGCTGTTGTTATTG 1659

RESULT 12

US-10-072-012-273

; Sequence 273, Application US/10072012

; Publication No. US2004003493A1

; GENERAL INFORMATION:

; APPLICANT: Tchernev, Velizar

; APPLICANT: Spytek, Kimberly

; APPLICANT: Zerhusen, Bryan

; APPLICANT: Patturajan, Meera

; APPLICANT: Shinkets, Richard

; APPLICANT: Li, Li

; APPLICANT: Gangolli, Esha

; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Anderson, David W.

; APPLICANT: Rastelli, Luca

; APPLICANT: Miller, Charles E.

; APPLICANT: Gerlach, Valerie

; APPLICANT: Taupier Jr, Raymond J.

; APPLICANT: Gusev, Vladimir Y.

; APPLICANT: Colman, Steven D.

; APPLICANT: Wolenc, Adam R.

; APPLICANT: Pena, Carol E. A

; APPLICANT: Furtak, Katarzyna

; APPLICANT: Grosse, William M.

; APPLICANT: Alsobrook II, John P.

; APPLICANT: Lepley, Denise M.

; APPLICANT: Rieger, Daniel K.

; APPLICANT: Burgess, Catherine E.

; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-258

; CURRENT APPLICATION NUMBER: US/10/072,012

; CURRENT FILING DATE: 2002-01-31

; PRIOR APPLICATION NUMBER: 60/265,102

; PRIOR FILING DATE: 2001-01-30


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; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 273
; LENGTH: 1701
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-072-012-273

Query Match          95.8%; Score 1589.8; DB 17; Length 1701;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 1642; Conservative 0; Mismatches 2; Indels 21; Gaps 3;

QY 1 ATGTGGACATGGGGCCCTGACAACTGATCGCCAAACACCGCCTACCTGCGAGCCCGG 60
DB 19 ATGTGGACATGGGGCCCTGACAACTGATCGCCAAACACCGCCTACCTGCGAGCCCGG 78
QY 61 AAGCCCTGGACTGGACAGCAAGAGCTGACGGCGCGCGGTAGCCCTGCCCTGCC 120
DB 79 AAGCCCTGGACTGGACAGCAAGAGCTGACGGCGCGCGGTAGCCCTGCCCTGCC 138
QY 121 GGGCTGCGAGGGCTGCGCGAGCTCGCCAGAGCTGCTCCGAACTTCCACAGCCTGTGT 180
DB 139 GGGCTGCGAGGGCTGCGCGAGCTCGCCAGAGCTGCTCCGAACTTCCACAGCCTGTGT 198
QY 181 GAGCAGCAGCCCATCGCTCGCCGCTCTTCCTGAGCTTCCTAGCAGCAGTGCACAGTTC 240
DB 199 GAGCAGCAGCCCATCGCTCGCCGCTCTTCCTGAGCTTCCTAGCAGCAGTGCACAGTTC 258
QY 241 CGCAAGCGGCAACTTCTTAGAGACGTGCGAGAACTGGAGCTGGCGAGGAGGAGCC 300
DB 259 CGCAAGCGGCAACTTCTTAGAGACGTGCGAGAACTGGAGCTGGCGAGGAGGAGCC 318
QY 301 ACCAAGACAGCGCTGCGAGGGCTGGTGGCACTTGTGCGAGTGCCTGCCCGGG 360
DB 319 ACCAAGACAGCGCTGCGAGGGCTGGTGGCACTTGTGCGAGTGCCTGCCCGGG 378
QY 361 AACCCGCAACCTTCTCAGCAGCGCTGGCGCACTCAAGTGCAGCAGCAGCAGTGCAG 420
DB 379 AACCCGCAACCTTCTCAGCAGCGCTGGCGCACTCAAGTGCAGCAGCAGCAGTGCAG 438
QY 421 GAAGAGCGAGTGGCTGCAAGTACGCTGCGCAAGGCTGAGGCCCATGGCTTTTTCGAAGAG 480
DB 439 GAAGAGCGAGTGGCTGCAAGTACGCTGCGCAAGGCTGAGGCCCATGGCTTTTTCGAAGAG 498
QY 481 CAGCCCTTTAAGGATTTCTGACAGCGCTTCTAGCAAGTCTTCTGAGTGGAACTC 540
DB 499 CAGCCCTTTAAGGATTTCTGACAGCGCTTCTAGCAAGTCTTCTGAGTGGAACTC 558
QY 541 TTCGAGATGCAACAGTGTGACAGTACTTCACTGAGTTCAGAGTGTGCGGAAAGT 600
DB 559 TTCGAGATGCAACAGTGTGACAGTACTTCACTGAGTTCAGAGTGTGCGGAAAGT 618
QY 601 GGTTTGGGAGGTATGTGCCGTCCAGGTGAAACACCTGGGAAGATGTATGCTGTAAAG 660
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RESULT 13
US-09-802-117-3

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DB 619 GGTTTGGGAGGTA-----AAAAACATGGGAAGATGTATGCTGTAAG 663
QY 661 AAATGGGACAGAACGGCTGAAGAAAGAGTGGCGAAGATGGCTCTCTTTGGAAG 720
DB 664 AAATGGGACAGAACGGCTGAAGAAAGAGTGGCGAAGATGGCTCTCTTTGGAAG 723
QY 721 GAAATCTTTGGAGAGGTGACAGCCCTTTTCATTTCTCTCTGGCTATGCTTTGAGAGC 780
DB 724 GAAATCTTTGGAGAGGTGACAGCCCTTTTCATTTCTCTCTGGCTATGCTTTGAGAGC 783
QY 781 AAGACCCATCTCTGCTTGTATGAGCTGATGAATGGGGAGACCTCAAGTTCCACATC 840
DB 784 AAGACCCATCTCTGCTTGTATGAGCTGATGAATGGGGAGACCTCAAGTTCCACATC 843
QY 841 TACAAAGTGGGACAGCGTGGCTGGACATGAGCCGGTGTATCTTTACTCGGCCACAGATA 900
DB 844 TACAAAGTGGGACAGCGTGGCTGGACATGAGCCGGTGTATCTTTACTCGGCCACAGATA 903
QY 901 GCCTGTGGATGCTGCACCTGCATGAACCTCGGCATGCTATCGGGACATGAAGCCTGAG 960
DB 904 GCCTGTGGATGCTGCACCTGCATGAACCTCGGCATGCTATCGGGACATGAAGCCTGAG 963
QY 961 AATGTGCTTCTGGATGACCTCGGCAACTGACGTTTATCTGACCTGGGGCTGGCGTGGAG 1020
DB 964 AATGTGCTTCTGGATGACCTCGGCAACTGACGTTTATCTGACCTGGGGCTGGCGTGGAG 1023
QY 1021 ATGAAGGTGGCAAGCCCATCACCCAGAG--GGCTGGAACCAATGGTTTACATGGCTCT 1077
DB 1024 ATGAAGGTGGCAAGCCCATCACCCAGAGGCGGTGGAACTTGTATGCTGCTCT 1083
QY 1078 GAGATCTTAATGGGAAAGGTAACTTCTATCTCTGTGGACTGTTTGGCCATGGGATGC 1137
DB 1084 GAGATCTTAATGGGAAAGGTAACTTCTATCTCTGTGGACTGTTTGGCCATGGGATGC 1143
QY 1138 AGCATTTATGAATGGTTGCTGGAGCAACACCTTCAAGATTACAAGGAAAGTCAAGT 1197
DB 1144 AGCATTTATGAATGGTTGCTGGAGCAACACCTTCAAGATTACAAGGAAAGTCAAGT 1203
QY 1198 AAAGAGGATCTGAAGCAAGAACTCTGCAAGACAGAGTCAAAATTCAGCATGATACTTC 1257
DB 1204 AAAGAGGATCTGAAGCAAGAACTCTGCAAGACAGAGTCAAAATTCAGCATGATACTTC 1263
QY 1258 ACAGAGGAAAGCAAGATATTTGCAAGCTCTTCTGGCTTAAGAAACACAGAGCAAGCTTA 1317
DB 1264 ACAGAGGAAAGCAAGATATTTGCAAGCTCTTCTGGCTTAAGAAACACAGAGCAAGCTTA 1323
QY 1318 GGAAGC---AGAGAAAGTCTGATGATCCAGGAAACATCATTTCTTTAAACGATCAAC 1374
DB 1324 GGAAGCAGGAGAGAAAGTCTGATGATCCAGGAAACATCATTTCTTTAAACGATCAAC 1383
QY 1375 TTTCTCGCCCTGGAGAGCTGGCTTAATGAAACCCCATTTGTGCCAGACCTTCAGTGGTT 1434
DB 1384 TTTCTCGCCCTGGAGAGCTGGCTTAATGAAACCCCATTTGTGCCAGACCTTCAGTGGTT 1443
QY 1435 TATGCCAAAGACATGCTGTAATTTGATGATTTCTCTGAGGTTTCGGGGGTGGAATTTGAT 1494
DB 1444 TATGCCAAAGACATGCTGTAATTTGATGATTTCTCTGAGGTTTCGGGGGTGGAATTTGAT 1503
QY 1495 GACAAAGATAGAGTCTTCTCAAAAACCTTTGGGACAGTGTGTTCTTATAGCATGGCAG 1554
DB 1504 GACAAAGATAGAGTCTTCTCAAAAACCTTTGGGACAGTGTGTTCTTATAGCATGGCAG 1563
QY 1555 GAAGAAATTAAGAAACGGGACTGTTTCAGGAACTGAAATGACCCCAACAGACCTACGGGT 1614
DB 1564 GAAGAAATTAAGAAACGGGACTGTTTCAGGAACTGAAATGACCCCAACAGACCTACGGGT 1623
QY 1615 TGTGAGGAGGTAAATTCATCAAGTCTGGCGTGTGTTTGTATTG 1659
DB 1624 TGTGAGGAGGTAAATTCATCAAGTCTGGCGTGTGTTTGTATTG 1668
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QY 301 ACCAAGACAGCGCGCTGAGGGGCTGTGGCCACTTGTGCAGTGCCTCCCTCCCGGG 360
Db 301 ACCAAGACAGCGCGCTGAGGGGCTGTGGCCACTTGTGCAGTGCCTCCCTCCCGGG 360
QY 361 AACCCGCAACCCCTTCTCAGCAGCGCGTGGCCACCAAGTGCACAGCAGCCACCACTGAG 420
Db 361 AACCCGCAACCCCTTCTCAGCAGCGCGTGGCCACCAAGTGCACAGCAGCCACCACTGAG 420
QY 421 GAAGAGCGAGTGGCTGCACTGACGCTGCGCAAGGCTGAGGCCCATGGCTTTCTTGAAGAAG 480
Db 421 GAAGAGCGAGTGGCTGCACTGACGCTGCGCAAGGCTGAGGCCCATGGCTTTCTTGAAGAAG 480
QY 481 CAGCCCTTTAAGGATTTCTGACAGCGCTTCTAGCAAAAGTTTCTGCAAGTGGAACTC 540
Db 481 CAGCCCTTTAAGGATTTCTGACAGCGCTTCTAGCAAAAGTTTCTGCAAGTGGAACTC 540
QY 541 TTCGAGATGCAACAGTGTGACAGCAAGTACTTCACTGAGTTCAGAGTGTGGGGAAGGT 600
Db 541 TTCGAGATGCAACAGTGTGACAGCAAGTACTTCACTGAGTTCAGAGTGTGGGGAAGGT 600
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QY 901 GCCTGTGGATGCTGCACCTCCATCACTCGCATCGCTATCGGGACATGAAGCTGAG 960
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RESULT 15

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; Sequence 3, Application US/09964469
; Patent No. US2002034803A1
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000636DIV
; CURRENT APPLICATION NUMBER: US/09/964,469
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 60/208,331
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: 09/738,894
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FaSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 36651
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; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(36651)
; OTHER INFORMATION: n = A,T,C or G
US-09-964-469-3
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Best Local Similarity 96.8%; Pred. No. 8.5e-176;
Matches 630; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 11, 2005, 00:47:58 ; Search time 258 Seconds
(without alignments)
3507.213 Million cell updates/sec

Title: US-10-044-205A-2

Perfect score: 2883

Sequence: 1 MVDGALDNLNTAYLQAR.....NRPTGCEGNSKSGVCLLL 553

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2883	99.8	1662	4	US-10-217-745-1
3	2883	99.8	2249	3	US-09-802-117-5
4	2883	99.8	2249	4	US-10-217-745-5
5	2876	99.6	1662	3	US-09-738-894A-1
6	2876	99.6	1662	4	US-09-964-469-1
7	1801	62.3	1062	3	US-09-802-117-3
8	1801	62.3	1062	4	US-10-217-745-3
9	1528	52.9	36651	3	US-09-738-894A-3
10	1528	52.9	36651	4	US-09-964-469-3
11	1280.5	44.3	2113	4	US-09-614-748A-7
12	1252.5	43.4	2511	4	US-09-417-197-60

13	1252.5	43.4	2529	4	US-09-417-197-42	Sequence 42, Appl
14	1252.5	43.4	2557	4	US-09-016-434-1298	Sequence 1298, Ap
15	1250.5	43.3	1975	4	US-09-614-748A-9	Sequence 9, Appl
16	1243.5	43.0	2017	4	US-09-614-748A-8	Sequence 8, Appl
17	1240	42.9	2848	3	US-08-464-954A-2	Sequence 2, Appl
18	1238	42.9	2204	1	US-08-221-817-12	Sequence 12, Appl
19	1238	42.9	2204	1	US-08-454-439-12	Sequence 12, Appl
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21	1236.5	42.8	2557	3	US-08-464-954A-1	Sequence 1, Appl
22	1210.5	41.9	1879	4	US-09-614-748A-10	Sequence 10, Appl
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24	1209.5	41.9	2206	1	US-08-221-817-10	Sequence 10, Appl
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28	1189	41.2	1983	1	US-08-454-439-21	Sequence 21, Appl
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30	1023.5	35.4	1420	4	US-09-614-748A-11	Sequence 11, Appl
31	991.5	34.3	1305	4	US-09-614-748A-12	Sequence 12, Appl
32	725.5	25.1	2362	4	US-09-620-312D-273	Sequence 273, App
33	725.5	25.1	3628	4	US-09-949-016-4773	Sequence 1306, Ap
34	721.5	25.0	2067	4	US-09-016-434-1306	Sequence 1312, Ap
35	678	23.5	3422	4	US-09-949-016-1312	Sequence 1735, Ap
36	509.5	17.6	2396	4	US-09-949-016-1735	Sequence 1471, Ap
37	507	17.5	3255	4	US-09-016-434-1471	Sequence 2007, Ap
38	507	17.5	6102	4	US-09-949-016-2007	Sequence 839, App
39	493	17.1	2705	4	US-09-949-016-839	Sequence 1959, Ap
40	493	17.1	2715	4	US-09-949-016-1959	Sequence 3, Appl
41	493	17.1	2754	3	US-09-429-322-3	Sequence 3, Appl
42	473.5	16.4	2274	4	US-09-772-647-3	Sequence 5704, Ap
43	473	16.4	2499	4	US-09-949-016-5704	Sequence 6, Appl
44	472.5	16.4	2324	4	US-09-190-976B-6	Sequence 1, Appl
45	469	16.2	2104	3	US-09-313-930-1	

ALIGNMENTS

RESULT 1
US-09-802-117-1
; Sequence 1, Application US/09802117
; Patent No. 644456

; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 644456 Human G-Coupled Protein Receptor Kinases and Polyn
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0147-USA
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US/09/802,117
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-802-117-1

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Score: 2883.00 Matches: 552
Percent Similarity: 99.82% Conservative: 0
Best Local Similarity: 99.82% Mismatches: 1
Query Match: 99.79% Indels: 0
DB: 3 Gaps: 0

US-10-044-205A-2 (1-553) x US-09-802-117-1 (1-1662)

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DB 1201 GAGGATCTGAAGCAAGAACTCTGCAAGACAGAGTCAAAATTCAGCATGATACTTCCACA 1260
QY 421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
DB 1261 GAGGAAGCAAAAGATATTTGAGGCTCTTCTTGCTGAAGAAACAGAGCAACGCTTAGGA 1320
QY 441 SerArgGluLysSerAspAspProArgLysHisPhePheLysThrIleAsnPhePro 460
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RESULT 2

US-10-217-745-1
; Sequence 1, Application US/10217745
; Patent No. 6838275
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6838275el Human G-Coupled Protein Receptor Kinases and
; TITLE OF INVENTION: Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/10/217,745
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US/09/802,117
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-217-745-1

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Query Match:	99.73%	Indels:	0
DB:	4	Gaps:	0

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Db 1261 GAGGAAGCAAAAGATATTTGTCAGGCTCTTCTGGCTAAGAAACACGAGACGCTTAGGA 1320
Qy 441 SerArgGluLysSerAspAspProArgLysHisPhePheLysThrIleAsnPhePro 460
Db 1321 AGCAGAGAAAAGTCTGATGATCCCGAGGAAACATCATTTCTTTAAACCATCAACTTCTCT 1380
Qy 461 ArgLeuGluAlaGlyLeuIleGluProPheValProAspProSerValValTyrAla 480
Db 1381 CGCTTGGAGTGGCTTAATTGAACCCCATTTGTGCCAGACCTTCACTGTTGTTATGCC 1440
Qy 481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
Db 1441 AAAGACATCGCTGAAATTTGATGATTTCTCTGAGGTTGCGGGGTGGAATTTGATGACAAA 1500
Qy 501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGlu 520
Db 1501 GATAAGCAGTTCTTTCAAAAACCTTTGCGACAGGTGCTGTCTATAGCATGCGGAGAAA 1560
Qy 521 IleIleGluThrGlyLeuPheGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
Db 1561 ATTATAGAAACGGGACTGTTTGAGGAAGTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
Qy 541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
Db 1621 GAGGTAATTCATCCAAAGTCTGGCGTGTGTTGTTATTG 1659

RESULT 3
US-09-802-117-5
; Sequence 5, Application US/09802117
; Patent No. 644456
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 644456el Human G-Coupled Protein Receptor Kinases and Polynu
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/09/802,117
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/188,449
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2249
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-802-117-5

Alignment Scores:
Pred. No.: 0 Length: 2249
Score: 2893.00 Matches: 552
Percent Similarity: 99.82% Conservative: 0
Best Local Similarity: 99.82% Mismatches: 1
Query Match: 99.79% Indels: 0
DB: 3 Gaps: 0

US-10-044-205A-2 (1-553) x US-09-802-117-5 (1-2249)

Qy 1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
Db 354 ATGTGGACATGGGGGCGCCCTGACAACTGTATGCGCAACCTGATGCGCAACCGCTACCTGACGCGCGG 413
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21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgSerLeuAlaLeuPro 40
414 AAGCCCTCGGACTGGACAGCAAGAGCTGCAGCGCGCGCGCTAGCCTGGCCCTGCC 473
41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLysCys 60
474 GGGCTGCAGGGCTGCGCGAGCTCCGCCAGAGCTGTCCCTGAACTTCCACAGCCTGTGT 533
61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
534 GAGCAGCAGCCATCGGTGCGCGCTCTTCCTGCGTACCTTCCTAGCCACAGTGCACCGTTC 593
81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
594 CGCAAGCGCGCAACCTTCCTAGAGACGTGCAGAACTGGGAGCTGGCCGAGAGGGACCC 653
101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
654 ACCAAAGACAGCGCTGCAGGGCTGTGTGCCACTTGTGCGAGTGCCTGCCCTGCCCGGG 713
121 AsnProGlnProPheLeuSerGlnAlaAlaThrLysCysGlnAlaAlaThrThrGlu 140
714 AACCGCAACCTTCCTCAGCGAGCGCTGCCCAAGTGCACAGCAGCCACCACTGAG 773
141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
774 GAAGACGAGTGGCTGCAGTACGCTGGCCAAAGCTGAGGCCATGGCTTCTTGCAAGAG 833
161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
834 CAGCCCTTTAAGGATTCGTGACCAAGCGCTTCTACGACAAGTTTCTGCAAGTGGAACTC 893
181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
894 TTCAGATGCAACACCAAGTGCAGCAAGTACTTCACTGAGTTCAGAGTGTGGGGAAGGT 953
201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
954 GGTTCGGGAGTATGTGCTCCAGTGAANAACACTGGGAAGATGATGCTGTGAAG 1013
221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyLysMetAlaLeuLeuLys 240
1014 AAATGGCAAGAGCGCTGAAGAAGAAAGTGGCGAAGATGGCTCTCTTGGANAAG 1073
241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
1074 GAAATCTTGGAGAGTCAAGAGCCCTTTCATGTCTCTCGCCCTATGCCCTTGGAGAGC 1133
261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLysPheHisIle 280
1134 AAGACCATCTCTGCTTGCATGAGCCTGATGATGGGGAGACCTCAAGTTCCACATC 1193
281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerIleGlnIle 300
1194 TACAAGTGGCAGCGCTGCGCTGGACATGAGCCGGGTGATCTTTTACTCGGCCAGATA 1253
301 AlaCysGlyMetLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
1254 GCTGTGGGATGCTGCACCTCCATGAACTCGGCATCTCTATCGGCACATGAAGCCTGAG 1313
321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
1314 AATGTCTTCTGATGACCTCGCAACTCGAGCTTATCTGACCTGGGGCTGGCGGTGGAG 1373
341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
1374 ATGAAGGGTGGCAAGCCCATCCCAAGGGGTGGAAACCAATGTTTACATGGCTCTCTGAG 1433
361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
1434 ATCTTAATGGAAGAGTAAGTATTCCTATCTCTGTGAGCTGGTTTCCATGGATGACAC 1493
381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400

1494 ATTTATCAATGCTGTGTCGACGAACACCACTTCAAGGAAAAGGTCAAGTAAA 1553
401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
1554 GAGGATCTGAAGCAAGAACTCTGCAAGACGAGGTCAATTCAGCANTGATTAATTTCACA 1613
421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
1614 GAGGAGCAAAAGATATTTGACGCTCTTCTGGTAAAGAAACAGAGCAACGCTTAGGA 1673
441 SerArgGluLysSerAspAspProArgLysHisPhePheLysThrIleAsnPhePro 460
1674 AGCAGAGAAAAGTCTGATGATCCAGGAAACATCTTCTTTAAACGATCAACTTTTCT 1733
461 ArgLeuGluAlaGlyLeuIleGluProPheValProAspProSerValValTyrAla 480
1734 CGCTGGAAGCTGCCCTAAATTGAACCCCAATTTGTGCCACACCTTCAGTGGTTATGCC 1793
481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
1794 AAAGACATCGCTGAAATTGATGATTTCTGAGGTTCCGGGGTGGAAATTTGATGACAAA 1853
501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTyrGlnGluGlu 520
1854 GATAAGCAGTTCTTCAAAAACTTTTGCACAGGCTGCTTCTTATAGCATGGCAGGAAGA 1913
521 IleIleGluThrGlyLeuPheGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
1914 ATTTAGAAACGGGACCTGTTGAGAACTGATGACCCCAACACACCTACGGGTGTGAG 1973
541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
1974 GAGGTAATTCATCAAGTCTGGGCTGTGTTGTTATTG 2012

RESULT 4

US-10-217-745-5
; Sequence 5, Application US/10217745
; Patent No. 6838275
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6838275: Human G-Coupled Protein Receptor Kinases and
; TITLE OF INVENTION: Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/10/217,745
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US/09/802,117
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2249
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-217-745-5

Alignment Scores:

Pred. No.:	0	Length:	2249
Score:	2883.00	Matches:	552
Percent Similarity:	99.82%	Conservative:	0
Best Local Similarity:	99.82%	Mismatches:	1
Query Match:	99.79%	Indels:	0
DB:	4	Gaps:	0

US-10-044-205A-2 (1-553) x US-10-217-745-5 (1-2249)

QY 1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrIleuGlnAlaArg 20
DB 354 ATGGTGGACATGGGGGCTCGACAACTGATCGCAACACCGCCTACCTGAGCCCGG 413

QY 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
DB 414 AAGCCCTCGGACTGCGACAGCAAGAGCTGCGAGCGCGCGGTAGCTGGCCCTGGCCC 473
QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
DB 474 GGGCTGCGAGGCTGCGCGAGCTCGCCAGAGCTGTCCCTGAACTTCCACAGCCCTGTGT 533
QY 61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
DB 534 GAGCAGCAGCCCATCGCTCGCGCCCTCTTCCTGAGCTTCCTAGCCACAGTGCACAGTTC 593
QY 81 ArgLysAlaAlaThrPheLeuLeuAspValGlnAsnThrGluLeuAlaGluGluPro 100
DB 594 CGCAAGCGCGCAACCTCTCTAGAGACGTCGCGAAGCTGGGAGCTGGCGAGAGGAGCC 653
QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
DB 654 ACCAAGACAGCGCGCTGCGAGGCTGTGTGCGACCTGTGTGAGTGGCCCTGGCCCGGG 713
QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
DB 714 AACCGCAACCTCTCTCAGCGAGCGCTGCGCAAGCTGAGGCGCATGGCTTTCTTGCAGAG 833
QY 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
DB 774 GAAGAGCAGTGGCTGCGAGTACGCTGCGCAAGCTGAGGCGCATGGCTTTCTTGCAGAG 833
QY 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnThrLysLeu 180
DB 834 CAGCCCTTTAGGATTTCTGTACCGAGCGCTTCTACGACAGTTTCTGAGTGGAACTC 893
QY 181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
DB 894 TTCGAGATGCAACAGCTGTCAGCAAGTACTTCACTGAGTTTCAGAGTCTGGGAAAGGT 953
QY 201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
DB 954 GGTTTTGGGAGGTATGTGCGCTCAGGTGAAACACTGGGAAGATGATGCTGTGAAG 1013
QY 221 LysLeuAspLysAlaLeuLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
DB 1014 AACTGGACAGAGCGCTGAGAGAAAGGTGGCGAGAGATGGCTCTCTTGGAAAG 1073
QY 241 GluLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
DB 1074 GAATCTTTGGAGAGGTGAGCAGCCCTTTCATTTGCTCTCTGGCTATGCTTTGAGAGC 1133
QY 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyLysAspLeuLysPheHisIle 280
DB 1134 AAGACCCATCTCTGCTTTGTATGAGCTGTATGATGAGGGGAGACCTCAAGTTCCACATC 1193
QY 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
DB 1194 TACAACGTGGGACGCGTGGCTGGACATGAGCGGGGTATCTTTACTCGGCCAGATA 1253
QY 301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
DB 1254 GCCTGTGGATGCTGCACCTCCATCACTCGGCATCGTCTATCGGACATGAGCCCTGAG 1313
QY 321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
DB 1314 AATGTCTTCTGGATGACCTCGGCAACTGCAAGTTATCTGACCTGGGCTGGCGCTGGAG 1373
QY 341 MetLysGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
DB 1374 ATGAAGGTGGAGAGCCCATCCCGAGAGGCTGGAACTATGTTATCATGGCTCTCTGAG 1433
QY 361 IleLeuMetGluLysValSerTyrSerTyrProValAspTyrPheAlaMetGlyCysSer 380
DB 1434 ATCTTATGGAAGAGTAAATTTCTCTATCTGTGGATCTGGTTGGCATGGGATGACG 1493
QY 381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400

DB 1494 ATTTATGAAATGGTTGCTGGACGAACACCATTTCAAAGATTCAAAGAAAGGTCAGTAAA 1553
QY 401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
DB 1554 GAGGATCTGAAGCAAGAACTCTCAAGACGAGGTCAAAATCCAGCATGATAACTTCACA 1613
QY 421 GluLysAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
DB 1614 GAGGAAGCAAAAGATATTTGAGGCTCTTTGCGCTAAAGAAACAGAGCAAGCTTAGGA 1673
QY 441 SerArgGluLysSerAspAspProArgLysHisPhePheLeuThrIleAsnPhePro 460
DB 1674 AGCAGAGAAAGTCTGATGATCCCGAGAAACATCATTTCTTTAAACCATCACTTCTCT 1733
QY 461 ArgLeuGluAlaGlyLeuIleGluProPheValProAspProSerValValTyrAla 480
DB 1734 CGCCTGGAAGCTGGCTTAATTTGAACCCCACTTTGTCGACAGCCCTTCAGTGGTTATGCC 1793
QY 481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
DB 1794 AAAGACATCGCTGAAATTTGATGATTTCTCTGAGGTTCCGGGGGTGGAATTTGATGACAAA 1853
QY 501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaThrGlnGluGlu 520
DB 1854 GATAAGCAGTTCCTTCAAAACCTTTTGGCAGAGTGTCTTCTATAGCATGGCAGGAAGAA 1913
QY 521 IleIleGluThrGlyLeuPheGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
DB 1914 ATTTATGAAACGAGACTGTTTGAAGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1973
QY 541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
DB 1974 GAGGTAATTCATCAAGTCTGGGCTGTGTTGTTATTG 2012

RESULT 5

US-09-738-894A-1
; Sequence 1, Application US/09738894A
; Patent No. 6331423
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO00636
; CURRENT APPLICATION NUMBER: US/09/738,894A
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Human
US-09-738-894A-1

Alignment Scores:
Pred. No.: 0 Length: 1662
Score: 2876.00 Matches: 551
Percent Similarity: 99.64% Conservative: 0
Best Local Similarity: 99.64% Mismatches: 2
Query Match: 99.55% Indels: 0
DB: 3 Gaps: 0

US-10-044-205A-2 (1-553) x US-09-738-894A-1 (1-1662)

QY 1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20

DB 1 ATGTGGACATGGGGGCCCTGACAACTGATCGCAACACCGCTACTCTGAGCCCGG 60

QY 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgSerLeuAlaLeuPro 40

DB 61 AAGCCCTCGGACTCGGACAGCAAGAGCTGAGCGGGCGGTAGCTTGCCCTTGCCC 120

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QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
Db 121 GGGCTGACAGGCTCGCGAGACTCGGCAGAAAGCTGTCCTTGAATCTTCCACAGAGCTGTGT 180
QY 61 GluGlnGlnProLysLeuArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
Db 181 GAGCAGCAGCCCATCGCTCGCGCTCTTCTCGTGACTTCTTAGCCACAGTGCCTCACGTTTC 240
QY 81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
Db 241 CGCAAGCGCGCAACCTTCTTAGAGAGAGCTGAGAACTGGGAGCTGGCGAGAGAGGAGCCC 300
QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
Db 301 ACCAAAGACAGCGGCTCGAGGGCTGTGGCCACTTGTGCGAGTGGCCCTGCCCCCGGG 360
QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
Db 361 AACCCGCAACCTTCTTCAGCCAGCGCTGGCCACCAAGTGCAGAGCAGCCACCACTGAG 420
QY 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
Db 421 GAAGAGCAGTGGCTGCAGTACGCTGGCCCAAGCTGAGGCCATGGCTTTCTTGCAGAG 480
QY 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
Db 481 CAGCCCTTTAAGGATTTCGTGACCGAGCCCTTCTACGACAGATTCTCGACTGGAACTC 540
QY 181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
Db 541 TTCGAGTGCACCAAGTGTGCAGAACGTTCTCACTGAGTTTCAGAGTCTGGGAAAGGT 600
QY 201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
Db 601 GGTTTTGGGAGGTATGTGCGCTCCAGGTGAAACACTGGGAAGATGTATGCCCTGTAAAG 660
QY 221 LysLeuAspLysLeuArgLeuLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
Db 661 AACTGGHACAGACGCTGAGAGAAAGGTGGCGAGAGATGGCTCTCTTGGAAAG 720
QY 241 GluLeuLeuGluLysValSerProPheLeuValSerLeuAlaTyrAlaPheGluSer 260
Db 721 GAAATCTTGGGAAGGTGACAGGCTTTCATTGTCTCTGGCTATGCTCTTTCAGAGC 780
QY 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
Db 781 AAGACCCATCTCTGCTTGTATGACCTGTATGAAATGGGGAGACCTCAAGTTTCCATC 840
QY 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
Db 841 TACAACGTGGGACAGCGTGGCTGGACATGAGCCGGGTGATCTTTTACTCGGCCAGATA 900
QY 301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
Db 901 GCCTGTGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960
QY 321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
Db 961 AATGTGCTTCTGGATGACCTCGCAACTGACAGTTATCTGACCTGGGGCTGGCGGTGAG 1020
QY 341 MetLysGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
Db 1021 ATGAAGGTGGCAGGCCCATCACCCAGAGGGCTGGAACTGGTTACATGGCTCCTGAG 1080
QY 361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
Db 1081 ATCTTAATGGGAAGGTAAGTTATCTTATCTCTGTGGACTGTTTGGCATGGGATGCAGC 1140
QY 381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
Db 1141 ATTTATGAATGGTTGCTGGAGCAACACCATTTCAAGATTACAGGAAGAAGGTCTAGTAA 1200
QY 401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
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Db 1201 GAGGATCTGAAGCAAGAACTCTGCAAGACGAGTCAAAATTCAGCATGATACTTCA 1260
QY 421 GluGluAlaLysAspLysCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
Db 1261 GAGGAAGCAAAAGATATTTGCGAGCTCTTCTTGCTGAAGAACCCAGAGCAACGCTTAGGA 1320
QY 441 SerArgGluLysSerAspProArgLysHisPheLysThrIleAsnPhePro 460
Db 1321 AGCAGAGAAAGTCTGATGATCCAGGAACAATCATTTCTTTAAACGATCACTTTCT 1380
QY 461 ArgLeuGluAlaGlyLeuIleGluProPheValProPheValProSerValValTyrAla 480
Db 1381 CGCTCGAAGCTGCGCTAAATTGAACCCCAATTTGTGCAGACCCCTTCAGTGGTTTATGCC 1440
QY 481 LysAspLysAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
Db 1441 AAAGACATCGCTGAAATTTGATATTTCTCTGAGGTTTCGGGGGGTGGAAATTTGATGACAAA 1500
QY 501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu 520
Db 1501 GATTAAGCAGTTCTTCAAAAACCTTTGCGACAGGTGCTGTTCTATAGCATGCGAGGAAGA 1560
QY 521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
Db 1561 ATTATAGAAACGGGACTGTTTGAAGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
QY 541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
Db 1621 GAGGTAATTATCATCAAGTCTGGCGGTGTGTTGTTATTTG 1659

RESULT 6
US-09-964-469-1
; Sequence 1, Application US/09964469
; Patent No. 6579709
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: CL000636DIV
; CURRENT APPLICATION NUMBER: US/09/964,469
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 60/208,331
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: 09/738,894
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Human
US-09-964-469-1

Alignment Scores:
Pred. No.: 0 Length: 1662
Score: 2876.00 Matches: 551
Percent Similarity: 99.64% Conservative: 0
Best Local Similarity: 99.64% Mismatches: 2
Query Match: 99.55% Indels: 0
DB: 4 Gaps: 0

US-10-044-205A-2 (1-553) x US-09-964-469-1 (1-1662)
QY 1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
Db 1 ATGGTGGACATGGGGGCCCTTGACAACTGATCGCAACCGCCCTACTCGAGGCCCGG 60
QY 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgSerLeuAlaLeuPro 40
Db 61 AAGCCCTCGACTGCGACAGCAAGAGCTGCAGCGCGCGGTAGCCTGCGCCCTGCCCC 120
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QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
DB 121 GGGCTGCGAGGCTGGCGAGCTCGCCAGAGAGCTGTCCTGAACTTCCACAGCCTGTGT 180
QY 61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
DB 181 GAGCAGCAGCCCATCGTCCGCGCTCTTCCTGAGCTTCTAGCCACAGTGCCTCAGTTTC 240
QY 81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGlyPro 100
DB 241 CGCAAGGCGCAACCTTCTAGAGAGCGTGCAGAACTGGGAGCTGGCCGAGGAGGACCC 300
QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
DB 301 ACCAAAGACAGCGCGCTGCAGGGCTGTGTGGCCACTTGTGCGAGTGCCTGCCCGGG 360
QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
DB 361 AACCCGCAACCTTCTCAGCCAGGCGGTGGCCACCAAGTGCAAGCAGCCACCACTGAG 420
QY 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
DB 421 GAAGAGCGAGTGGCTGCAGTGCAGCTGGCCAAAGGCTGAGGCCATGGCTTCTTGCAGAG 480
QY 161 GlnProPheLysAspPheValThrSerAlaPheThrAspLysPheLeuGlnTrpLysLeu 180
DB 481 CAGCCCTTTAAGGATTTCTGACCAAGCGCTTCTACGACAAGTTTCTGCAAGTGGAAATC 540
QY 181 PheGluMetGlnProValSerAspLysThrPheThrGluPheArgValLeuGlyLysGly 200
DB 541 TTCGAGATGCAACCAAGTGTACACAAGTACTTCTCAGTGTGCTGAGAGTGTGGGGAAGGT 600
QY 201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyraLysLys 220
DB 601 GGTTTGGGAGGTATGTGCCCTCAGGTGAAACACATGGGAAGATGATGCTGTAAG 560
QY 221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyLysMetAlaLeuLeuGluLys 240
DB 661 AAATCGCAACAAGCGGCTGAAGAAGAAAGGTGGCGAAGATGGCTCTCTTGGAAAG 720
QY 241 GluLeuGluLysValSerSerProPheIleValSerLeuAlaThrAlaPheGluSer 260
DB 721 GAAATCTTGGAGAAGTCAAGAGCCCTTCTCATGTCTCTCGCCCTATGCTTTCAGAGC 780
QY 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
DB 781 AAGACCCATCTGCTGCTGATGAGCTGATGATGGGGAGACCTCAAGTTCACATC 840
QY 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheThrSerAlaGlnIle 300
DB 841 TACAACGTGGGCAGCGCTGGCTGACATGAGCGGGTGATCTTTTACTCGGCCACAGATA 900
QY 301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
DB 901 GCCTGGGATGCTGCACCTCATGAACCTCGGCATCGTCTATCGGACATGAAGCCTGAG 960
QY 321 AsnValLeuLeuAspLeuGlyAsnCysArgLysSerAspLeuGlyLeuAlaValGlu 340
DB 961 AATGTCTTCTGATGACCTCGGCACTCGAGTTATCTGACCTGGGGCTGGCCGTGAG 1020
QY 341 MetLysGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
DB 1021 ATGAAGGGTGGCAAGCCCATCCAGAGGGCTGGAACCAATGTTTACATGGCTCCTGAG 1080
QY 361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
DB 1081 ATCTTAATGGGAAGAGTAAATTTATTTCTTCTATCTGTGGACTGTTTGGCCATGGGATGCAGC 1140
QY 381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
DB 1141 ATTTATGAATGGTGTGGAGCAACACCATTTCAAGATTACAGAAAGTTCAGTAAA 1200
QY 401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420

DB 1201 GAGGATCTGAAGCAAGAACTCTGCAAGACGAGGTCAAATTCAGCATGTATACTTCACA 1260
QY 421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
DB 1261 GAGGAAGCAAGATATTTGAGGCTCTCTTGGCTAGAAACACAGAGCAAGCTTAGGA 1320
QY 441 SerArgGluLysSerAspAspProArgLysHisPhePheLysThrIleAsnPhePro 460
DB 1321 AGCAGAGAAAGTCTGATGATCCAGGAAACATCATTTCTTTAAACGATCAACTTTCCT 1380
QY 461 ArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValTyrAla 480
DB 1381 CGCTTGGGAAGCTGGCTTAATTTGAACCCCATTTGTGCCAGACCTTTCAGTGGTTATGCC 1440
QY 481 LysAspIleAlaGluLeuAspPheSerGluValArgGlyValGluPheAspAspLys 500
DB 1441 AAAGACATCGCTGAATTTGATGATTTCTGAGGTTCCGGGGGTGGAAATTTGATGACAAA 1500
QY 501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu 520
DB 1501 GATAGCAGTCTTCAAAAACCTTTCGACAGGCTGCTTCTTATAGCATGGCAGGAAGAA 1560
QY 521 IleIleGluThrGlyLeuPheGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
DB 1561 ATTATAGAAACGGGACTGTTTGGAGAACTGAATGATGATGATGATGATGATGATGAT 1620
QY 541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
DB 1621 GAGGTAATTAATCCAGTCTGGCGTGTTGTTGTTATTG 1659

RESULT 7

US-09-802-117-3
; Sequence 3, Application US/09802117
; Patent No. 6444456
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 644456el Human G-Coupled Protein Receptor Kinases and Polym
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/09/802,117
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/188,449
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-802-117-3

Alignment Scores:
Pred. No.: 3,7e-206 Length: 1062
Score: 1801.00 Matches: 349
Percent Similarity: 99.71% Conservative: 0
Best Local Similarity: 99.71% Mismatches: 1
Query Match: 62.34% Indels: 0
DB: 3 Gaps: 0

US-10-044-205A-2 (1-553) x US-09-802-117-3 (1-1062)

QY 1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
DB 1 ATGTGGTGCATGGGGCCCTGACAACTGATCGCCAAACACCGCTTACCTGCAGGCCCGG 60
QY 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
DB 61 AAGCCCTCGGACTGCGACAGCAAGAGCTGCAGCGCGCGCGGTAGCTTGGCCCTTGCCC 120
QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysSerLeuSerLeuAsnPheHisSerLeuCys 60

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Db 121 GGGGTGAGGCGTGGCGGAGCTCGCCGAGAGCTGCTCCCTGAACCTCCACAGCTGTGT 180
Qy 61 GluGlnGlnProIleGlyArgArgLeuPheArgPhePheLeuAlaThrValProThrPhe 80
Db 181 GAGCAGCAGCCATCGGTGCGCGCTCTTCGTGACTTCTTAGCCACAGTGCACAGCTTC 240
Qy 81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluPro 100
Db 241 CGCAAGGCGGCAACCTTCCTAGAGAGCTGCGGAGCTGGGAGCTGGCGAGAGGAGCCC 300
Qy 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
Db 301 ACCAAGACAGCGCGCTGACAGGCGTGGTGGCCACTTGTGGAGTGGCCCTGCCCGGG 360
Qy 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
Db 361 AACCCGCAACCTTCCTCAGCCAGCGCTGGCCACCAAGTGCACAGCAGCAGCAGCTGAG 420
Qy 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
Db 421 GAAGAGCGAGTGGCTGCAAGTACGCTGGCCAGGCTGAGGCGCATGGCTTTCTTGCAAG 480
Qy 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
Db 481 CAGCCCTTTAAGGATTTCTGTACCAAGCGCTTCTACGACAAAGTTTCTGCAGTGAACATC 540
Qy 181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGluLysGly 200
Db 541 TTCGAGATGCAACACAGTGTGACAAAGTACTTCACTGAGTTTCAGAGTCTCGGGAAAGGT 600
Qy 201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
Db 601 GGTTTTGGGAGGTATGTGCGCTCCAGTGAAGAAACATCTGGGAAAGTATGCTGTAAAG 660
Qy 221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGlyLysMetAlaLeuGluLys 240
Db 661 AAATGGACAAGCGGCTGAAGAAAGTGGCGAGAGATGGCTCTCTTGGAAAAG 720
Qy 241 GluLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
Db 721 GAAATCTTGGAGAAGGTGACAGCGCTTTCATTTGCTCTCTGGCTATGCTTTCGAGAGC 780
Qy 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLysPheHisIle 280
Db 781 AAGACCATCTCTGCTTGTGATGAGCTGATGATGGGGAGACCTCAAGTTCCACATC 840
Qy 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
Db 841 TACAACGTGGCAGCGCTGGCTGGACATGAGCGCGGTGATCTTTTACTCGGCCAGATA 900
Qy 301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
Db 901 GCCTGTGGATGCTGCACCTCATGAACCTGGCATCGTCTATCGGACATGAAGGCTGAG 960
Qy 321 AsnValLeuLeuAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
Db 961 ATGTGCTTCTGGATGACCTCGGCAACTGACAGTTATCTGACCTGGGGCTGGCGTGGAG 1020
Qy 341 MetLysGlyGlyLysProIleThrGlnArg 350
Db 1021 ATGAAGGGTGGCAAGCCCATCACCAGAGG 1050
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RESULT 8

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US-10-217-745-3
; Sequence 3, Application US/10217745
; Patent No. 6838275
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6838275el Human G-Coupled Protein Receptor Kinases and
; TITLE OF INVENTION: Polynucleotides
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; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/10/217,745
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US/09/802,117
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-217-745-3
Alignment Scores:
Pred. No.: 3,7e-206 Length: 1062
Score: 1801.00 Matches: 349
Percent Similarity: 99.71% Conservative: 0
Best Local Similarity: 99.71% Mismatches: 1
Query Match: 62.34% Indels: 0
DB: 4 Gaps: 0
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US-10-044-205A-2 (1-553) x US-10-217-745-3 (1-1062)

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Qy 1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
Db 1 ATGGTGCACATGGGGCGCTGGACAACTGATCGCAACACCGCTTACTCGAGCGCCGG 60
Qy 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgSerLeuAlaLeuPro 40
Db 61 AAGCCCTCGGACTCGACAGCAAGAGCTGCGGGCGCGGCTAGCTGGCCCTGGCC 120
Qy 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
Db 121 GGGCTGCAGGCTCGCGGAGCTCCGCCAGAAAGCTGCTCCCTGAACCTTCCACAGCTGTGT 180
Qy 61 GluGlnGlnProIleGlyArgArgLeuPheArgPhePheLeuAlaThrValProThrPhe 80
Db 181 GAGCAGCAGCCATCGGTGCGCGCTCTTCGTGACTTCTTAGCCACAGTGCACAGCTTC 240
Qy 81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluPro 100
Db 241 CGCAAGGCGGCAACCTTCCTAGAGAGCTGCGGAGCTGGCGAGCTGGCGAGGAGGCC 300
Qy 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
Db 301 ACCAAGACAGCGCGCTGACAGGCGTGGTGGCCACTTGTGGAGTGGCCCTGCCCGGG 360
Qy 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
Db 361 AACCCGCAACCTTCCTCAGCCAGCGCTGGCCACCAAGTGCACAGCAGCAGCAGCTGAG 420
Qy 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
Db 421 GAAGAGCGAGTGGCTGCAAGTACGCTGGCCAGGCTGAGGCGCATGGCTTTCTTGCAAG 480
Qy 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
Db 481 CAGCCCTTTAAGGATTTCTGTACCAAGCGCTTCTACGACAAAGTTTCTGCAGTGAACATC 540
Qy 181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGluLysGly 200
Db 541 TTCGAGATGCAACACAGTGTGACAAAGTACTTCACTGAGTTTCAGAGTCTGGGGAAAGGT 600
Qy 201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
Db 601 GGTTTTGGGAGGTATGTGCGCTCCAGTGAAGAAACATCTGGGAAAGTATGCTGTAAAG 660
Qy 221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGlyLysMetAlaLeuGluLys 240
Db 661 AAATGGACAAGCGGCTGAAGAAAGTGGCGAGAGATGGCTCTCTTGGAAAAG 720
Qy 241 GluLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
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721	GAAATCTTGAGAAGGTCAGAGCCCTTTTCATTGTCTCTCTGGCCTATGCTTTGAGAGC	780
261	LYeThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle	280
781	AAGACCCATCTCTGCCTTGTTCATGAGCCTCATGAATGGGGAGACCTCAAGTTCCACATC	840
281	TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle	300
841	TACAACGTGGGCACGCGCTGGCCCTGGACATGAGCGGGTGATCTTTTACTCGGCCACAGTA	900
301	AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu	320
901	GCCTGTGGGATGTCGCACCTCCATGAATCGGCATCGTCTATCGGGACATGAAGCCCTGAG	960
321	AsnValLeuLeuAspAspLeuGlyIleAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu	340
961	AATGTGCTCTTGATGACCTCGGCNACTGGCAGGTATTCGACCTGGGGCTGGCCGTGGAG	1020
341	MetLysGlyGlyLysProIleThrGlnArg	350
1021	ATGAAGGGTGGCAAGCCCATCACCAGAGG	1050

RESULTS

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US-09-738-894A-3
; Sequence 3, Application US/09738894A
; Patent No. 6331423
; GENERAL INFORMATION:
; APPLICANT: GURGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000636
; CURRENT APPLICATION NUMBER: US/09/738,894A
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 36651
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(36651)
; OTHER INFORMATION: n = A,T,C or G
US-09-738-894A-3

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Qy	81	ArgLysAlaAlaThrPheLeuGlnuAspValGlnAenTrpGluLeuAlaGluGlyPro	100
Db	2316	CGCAAGCGCGCAACCTTCCTAGAGACGTCGAGAACTGGGAGCTGGCGAGAGGAGCC	2375
Qy	101	ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly	120
Db	2376	ACCAAGACAGCGCTGCAGGGCTGGTGGCCACTTGTGCCAGTGCCCTGCCCCGGGG	2435
Qy	121	AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu	140
Db	2436	AACCCGCAACCTTCCTCAGCCAGCGCTGGCCACCAAGTGCCAAGCAGCCACCACTGAG	2495
Qy	141	GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu	160
Db	2496	GAAGAGCGAGTGGCTGCAGTCAGCTGGCGAAGGCTGAGGCCATGGCTTCTTTCGAAGAG	2555
Qy	161	GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu	180
Db	2556	CAGCCCTTTAAGGATTCGTGACCAGCGCTTCTACGACAAGTTCTTCAGGTGGAAACTC	2615
Qy	181	PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly	200
Db	2616	TTCCGAGTCACACCGAGTGTCAACAAGACTTCACTGAGTTCAGAGTGTCTGGGGAAGGT	2675
Qy	201	GlyPheGlyGlu	204
Db	2676	GGTTTTGGGGAGGTAAGTGTCTCCAGTAGCCAGGCTAGAGGTGAAGCATAGAGCATGA	2735
Qy	204	-----	204
Db	2736	AAGGGGGTAATGTGGCTTCTTTTAAATCTCAGTTACTTGAACCTAATTTCAGCAC	2795
Qy	204	-----	204
Db	2796	CATATGTGGAGGATTTCTAGCCCCGTCTCCCAGCCCCCTTCTTTGTGTGCCATGGTG	2855
Qy	204	-----	204
Db	2856	TGAATATAAAACAAATGGCATGAGAGACAAGCAAAATTTATCTTGGCCAAGACTCT	2915
Qy	204	-----	204
Db	2916	GTCATGGGTCTCCATTAGAACGTGCTGAGATGCTCGACACTTCAGAGAATGATAGCAA	2975
Qy	204	-----	204
Db	2976	TGTGTGACAGAAGATCTCGTTTCCCTTAATTTGTGATANTGAAGGCACCTTCAGAAAAA	3035
Qy	204	-----	204
Db	3036	TGGATATTTAAGAAAAATCTCTAACTAGCTGGGTGTGTGACATGCCTGTAATCCAGCT	3095
Qy	204	-----	204
Db	3096	ACTTGGGGGCTGAAGCAGAGAATCACTTGAGCCTGGGAGGTGGAGTTGCAGTGAGCC	3155
Qy	204	-----	204
Db	3156	AAGATCGTGCCACTGCATCTCAGCCCTGGGTGACAGAGCAAGCTCAAAAAA	3215
Qy	204	-----	204
Db	3216	AAGAAAGAAAGAAAGAAAGAAACACTTATCTTGAAGTAAGTTTGAGAACCTGTTTTGT	3275
Qy	204	-----	204
Db	3276	ACCACTGTTGCCAGCTTCTGTTTTTAAGTAATAAAAAATATTTCAGGTAAATTTG	3335
Qy	204	-----	204
Db	3336	CTTGATATAAACTAACCAATTAACTGTTTTTAAATGTTCATGTCAGTGGCACTTCGCACA	3395
Qy	204	-----	204

D	b	3396	AATGCAATGTTGGGTAA	GCAACACCTCAATCTGGAT	CCAAGACACTCTCATCACCCTGT	3455
Q	y	204	-----	-----	-----	204
D	b	3456	GCCATTAAATAGTGCCTCC	CCATCCCTCTCCTCCAGCCCTG	CAACCACTAGTCGCG	3515
Q	y	204	-----	-----	-----	204
D	b	3516	TTTCTGTCTTAGGGATT	TGCCTATTCTGGGTGTTT	CACAATATGTGACCTTTTGTGT	3575
Q	y	204	-----	-----	-----	204
D	b	3576	CTGGCTTCTTCACTCACT	ATTAGAAATGTTTTTGGGGT	TCAATTCACACTGTAGCATGTCAA	3635
Q	y	204	-----	-----	-----	204
D	b	3636	TACTCCATTTCTTTTAT	GGCTGTATAATAATTC	CATGTGGATGTACTACATTTTCATG	3695
Q	y	204	-----	-----	-----	204
D	b	3696	TAGCCATTCACTGTTG	ATGGACACTTGGGCTGTTT	CACCTTTGGCTATTGTGTATGG	3755
Q	y	204	-----	-----	-----	204
D	b	3756	TGTGCTATTCAATGACA	AGTAATTGTTTGAATCCT	TGTTTTCATTTCTCTTGGATTAT	3815
Q	y	204	-----	-----	-----	204
D	b	3816	GCCAGAGTGGAAATG	CTAGGGCATATGGTGATA	CTACTATGTTTAACTTTTCAAGGAGCCA	3875
Q	y	204	-----	-----	-----	204
D	b	3876	CCAAACTTCCACATTT	TTTATCCCAACAGCAATG	CTTAAAGTTTCGATTTCTCCACA	3935
Q	y	204	-----	-----	-----	204
D	b	3936	TCCTTGCCAAACACT	TGTGATATTTTCTCTGTA	TTTTTTTATGAAGCGTCCTAGTAGGTGA	3995
Q	y	204	-----	-----	-----	204
D	b	3996	AGGAGTATCGCACTG	TAGTCCCCACTTTTCT	TTCAGAACACTTCTTATTACAGTACTC	4055
Q	y	204	-----	-----	-----	204
D	b	4056	CTTCTCCAATGCTAAC	ATCTTTCCACCACCTCCT	CTCTTATCATCTCCACCTCTCTG	4115
Q	y	205	-----	-----	-----	205
D	b	4116	CAGTACCATTACTTCT	ACCTCTTCTCTCTTTT	CTTCTCCTTTTAAAGTATGTGCCGT	4175
Q	y	208	lGlnValLysAsnThr	GlyLysMetTyrAlaCys	LysLysLeuAspLysLysArgLeuLys	228
D	b	4176	CCAGGTGAAAAACACT	GGGAAGATGTATGCTGT	AGAAAACAGCAAGAAGCGCTGAA	4235
Q	y	228	sLysLysGlyGlyGlu	LysMetAlaLeuGluLys	GluLysGluLysValSerSe	248
D	b	4236	GAAGAAAGGTGGCGA	GAAGATGGCTCTCTTGG	AAAAAGGAAATCTTGAGAAGTCA	4295
Q	y	248	rProPheIleValSer	LeuAlaTyrAlaPheGlu	SerLysThrHisLeuCysLeuValMe	268
D	b	4296	CCCTTTTCATTGTCT	CTCTGSCCTATGCCTT	TGTAGAGCAAGACCCCACTCTG	4355
Q	y	268	tSerLeuMetAsnGly	LysAspLeuLysPheHis	IleTyrAsnValGlyThrArgGlyLe	288
D	b	4356	GAGCCTGATGAATGG	GGGAGACCTCAAGTTCC	ACATCTACACGTGGCGACGCGTGCCT	4415
Q	y	288	uAspMetSerArgVal	lIlePheTyrSerAlaGln	IleAlaCysGlyMetLeuHisLeuHi	308
D	b	4416	GGACATGAGCCGGT	GAATCTTTTACTCGGCC	CAAGATAGCCTGTGGGATGCTGCAC	4475
Q	y	308	sGluLeuGlyIleVal	TyrArgAspMetLysPro	GluAsnValLeuLeuAspLeuGlu	328

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Db      4476  TGAACCTCGGCATCGTCTATCGGCACATGAAGCCTGAGATGTGCTTCTGGATGACCTCGG 4533
Qy      328  YAsnCysArgLeuSerAspLeuGlyLeuAlaValGluMetLysGlyGlyLysProIleTh 348
Db      4536  CAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAGATGAAGGGTGGCAAGCCCATCAC 4595
Qy      348  xGlnAtg 350  |||||
Db      4596  CCAGAGG 4602

RESULT 10
US-09-964-469-3
; Sequence 3, Application US/09964469
; Patent No. 6579709
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000636DIV
; CURRENT APPLICATION NUMBER: US/09/964,469
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 60/208,331
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: 09/738,894
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 36651
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(36651)
; OTHER INFORMATION: n = A, T, C or G
US-09-964-469-3

Alignment Scores:
Pred. No.:      8,73e-171      Length:      36651
Score:          1528.00      Matches:      349
Percent Similarity: 41.40%      Conservative: 0
Best Local Similarity: 41.40%      Mismatches: 1
Query Match:      52.89%      Indels:      493
DB:              4          Gaps:      1

US-10-044-205A-2 (1-553) x US-09-964-469-3 (1-36651)
Qy      1  MetValaspMetGlyAlaLeuaspAsnLeuIleAlaAsnThrAlaThrIleuGlnAlaArg 20
Db      2076  ATCGTGGACATGGGGCCCTTGACAAACCTGATCGCCACACACCGCTACTGTGAGGCCCGG 2135
Qy      21  LysProSerAspCysAspSerLysGluLeuGlnArgArgArgSerLeuAlaLeuPro 40
Db      2136  AAGCCCTCGGATGCGACAGCAAGAGCTGCGAGCGCGGTAGCTGGCCCTGGCC 2195
Qy      41  GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
Db      2196  GGGCTCGAGGGCTGCGCGGAGCTCCGCCAAGAAGCTGCCTGAACTTCACAGCCTGTGT 2255
Qy      61  GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
Db      2256  GAGCAGACGCCCATCGGTGCGCGCCTCTTCCTGGTACTTCTTAGCCACAGTGGCCACGTTTC 2315
Qy      81  ArgLysAlaAlaThrPheLeuGluaspValGlnAsnTrpGluLeuAlaGluGlyPro 100
Db      2316  CGCAAGGCGCAACCTTCTTAGAGAGCGTGCAGAACTGGGACTGGCCGAGGAGGCC 2375
Qy      101  ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProIleGly 120
Db      2376  ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGGCCCTGCCCCGGG 2435
Qy      121  AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140

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Db 1636 CCCAAGAAAGGGCTGCTCCAGAGACTCTTCAAGCGGCAGC 1675
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RESULT 13

US-09-417-197-42

; Sequence 42, Application US/09417197

; Patent No. 6518021

; GENERAL INFORMATION:

; APPLICANT: Ole THASTRUP, et al.

; TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An

; FILE OF INVENTION: On A Cellular Response

; FILE REFERENCE: 3759-0110P

; CURRENT APPLICATION NUMBER: US/09/417,197

; CURRENT FILING DATE: 1999-10-07

; NUMBER OF SEQ ID NOS: 143

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 42

; LENGTH: 2529

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: EGFP-G-k5 fusion

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(2526)

US-09-417-197-42

Alignment Scores:

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Query Match:	43.35%	Indels:	50
DB:	4	Gaps:	11

US-10-044-205A-2 (1-553) x US-09-417-197-42 (1-2529)

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QY 133 LysCysGlnAlaAlaThrThrGluGluGluArgValAlaAlaValThrLeuArgLysAla 152
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QY 173 AspLysPheLeuGlnTrpLysLeuPheGluMetGlnProValSerAspLysTyrPheThr 192
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Db 1258 GACCGCTTCTCCAGTGGAGTGGTTGAAAGGCAACCGGTGACCAAAAAACACTTTCAGG 1317
QY 193 GluPheArgValLeuGlyLysGlyPheGlyGluValCysAlaValGlnValLysAsn 212
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QY 353 ThrAsnGlyTyrMetAlaProGluIleLeuMetGluLysValSerTyrSerTyrProVal 372
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Db 1855 GACTACTGGGCGCTTGGCTGCTCATCTATGAGATGATCGAGGGCCAGTCCGCTCCGC 1914
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QY 413 LysPheGlnHisAspAsnPheThrGluAlaLysAspIleCysArgLeuPheLeuAla 432
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QY 532 -----AspPro-AsnAr 535

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RESULT 14

US-09-016-434-1298
; Sequence 1298, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1298:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2557 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: G306804
US-09-016-434-1298

Alignment Scores:
Pred. No.: 1,31e-139 Length: 2557
Score: 1252.50 Matches: 259
Percent Similarity: 63.07% Conservative: 103
Best Local Similarity: 45.12% Mismatches: 162
Query Match: 43.35% Indels: 50
DB: 4 Gaps: 11

US-10-044-205A-2 (1-553) x US-09-016-434-1298 (1-2557)

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Qy 46 AlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCysGluGlnPhePro 55
Db 347 GAAGACCTCCCAAGAGGACCATAGACAGATTAATCTAGCTTTATGTGCAAGCAGCAATTC 406
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Db 467 TTCTCTGAGCTCGTGGCAGAAATATGAAGTTACTCCAGATGAAAAACTGGGAGAAAGGG 526
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Search completed: May 11, 2005, 06:59:43
Job time : 312 secs

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GenCore version 5.1.6
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Run on: May 11, 2005, 04:38:46 ; Search time 766 Seconds
(without alignments)
4418.383 Million cell updates/sec

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Perfect score: 2889
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Delop 6.0 , Delext 7.0

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Total number of hits satisfying chosen parameters: 11324664

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2889	100.0	2198	13	US-10-044-205A-1	Sequence 1, Appli
3	2883	99.8	1662	9	US-09-802-117-1	Sequence 1, Appli
4	2883	99.8	1662	14	US-10-217-745-1	Sequence 1, Appli
5	2883	99.8	1662	17	US-10-311-034-45	Sequence 45, Appl
6	2883	99.8	1662	17	US-10-451-168-49	Sequence 49, Appl
7	2883	99.8	1662	19	US-10-788-197-22	Sequence 22, Appl
8	2883	99.8	2249	9	US-09-802-117-5	Sequence 5, Appli
9	2883	99.8	2249	14	US-10-217-745-5	Sequence 5, Appli
10	2876	99.6	1662	9	US-09-964-469-1	Sequence 1, Appli
11	2876	99.6	1662	16	US-10-425-962-1	Sequence 1, Appli
12	2823.5	97.7	1701	17	US-10-072-012-273	Sequence 273, App
13	1801	62.3	1062	9	US-09-802-117-3	Sequence 3, Appli
14	1801	62.3	1062	14	US-10-217-745-3	Sequence 3, Appli
15	1528	52.9	36651	9	US-09-964-469-3	Sequence 3, Appli
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17	1283.5	44.4	1737	16	US-10-325-430-2	Sequence 2, Appli
18	1283.5	44.4	1737	19	US-10-788-197-18	Sequence 18, Appl
19	1283.5	44.4	2113	16	US-10-325-430-1	Sequence 1, Appli
20	1280.5	44.3	2113	19	US-10-677-983-7	Sequence 7, Appli
21	1268.5	43.9	1692	19	US-10-788-197-24	Sequence 24, Appl
22	1258	43.5	1683	19	US-10-788-197-6	Sequence 6, Appli
23	1258	43.5	1770	19	US-10-788-197-12	Sequence 12, Appl
24	1252.5	43.4	1773	19	US-10-788-197-12	Sequence 12, Appl
25	1252.5	43.4	2467	15	US-10-084-817-110	Sequence 110, App
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27	1252.5	43.4	2519	13	US-10-071-766-13	Sequence 13, Appl
28	1252.5	43.4	2529	14	US-10-072-036-42	Sequence 42, Appl
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34	1250.5	43.3	1599	19	US-10-788-197-20	Sequence 20, Appl
35	1250.5	43.3	1975	19	US-10-677-983-9	Sequence 9, Appli
36	1245.5	43.1	2519	10	US-09-971-392-72	Sequence 72, Appl
37	1243.5	43.0	1641	19	US-10-788-197-16	Sequence 16, Appl
38	1243.5	43.0	2017	19	US-10-677-983-8	Sequence 8, Appli
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ALIGNMENTS

RESULT 1
US-10-044-205A-3
; Sequence 3, Application US/10044205A
; Publication No. US20020123464A1
; GENERAL INFORMATION:
; APPLICANT: KAPILLER-LIBERMANN, Rosana
; APPLICANT: BANDARU, Rajasekhara
; TITLE OF INVENTION: 69087, 15821, and 15418, Methods and Compositions of Human Protei
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 10147-52U1
; CURRENT APPLICATION NUMBER: US/10/044,205A
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/242,428
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: US 60/241,884
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/241,877
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3
; LENGTH: 1659
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-044-205A-3

Alignment Scores:

Pred. No.: 0 Length: 1659
Score: 2889.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-044-205A-2 (1-553) x US-10-044-205A-3 (1-1659)

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QY 1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
DB 1 ATGGTGGACATGGGGGCGCTGGACAACTGATCGCAACACCGCTACCTGCAGGCCCGG 60
QY 21 LysProSerAspCysAspSerIlyysGluLeuGlnArgArgArgSerLeuAlaLeuPro 40
DB 61 AAGCCTCGACTCGACGACGAAAGAGCTGCAGCGCGCGCGCTAGCCTGCGCCCTGCC 120
QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPhHisSerLeuCys 60
DB 121 GGGCTGCAGGCGTGGCGGAGCTCGCCAGAAAGCTGTCCCTGAACTTCCACAGCCCTGT 180
QY 61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
DB 181 GAGCAGCAGCCCATCGCTCGCGCGCTTCCGTGACTTCTAGCCACAGTGCACACGTT 240
QY 81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTyrGluLeuAlaGluGluGlyPro 100
DB 241 CCACAGCGCGCACTTCTAGAGAGCTGCAGAACTCGGAGCTGCGCGAGAGGAGCC 300
QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
DB 301 ACCAAGACAGCGCTGCAGCGGCTGTGTGGCACTTGTGGAGTGCCTGCGCCCGGG 360
QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
DB 361 AACCGCAACCTTCTCAGCGAGCGCTGCGCAACCAAGTGCACAGCAGCCACCACTG 420
QY 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
DB 421 GAAGAGCAGTGGCTGCGAGTACGCTGCGAGAGCTGAGGCGCATGGCTTCTTGCAGAG 480
QY 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
DB 481 CAGCCCTTTAAGGATTTCTGTGACCAAGCGCTTCTACGACNAAGTTTCTGAGTGGAACT 540
QY 181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
DB 541 TTCGAGATGCACACAGTGCAGACAAAGTACTTCACTGAGTTTCTGAGTGTCTGGGAAAG 600
QY 201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
DB 601 GGTITTTGGGAGTATGTGCGCTCAGGTGAAACACTGGGAAGATGTATGCTCTGTAG 660
QY 221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGlyLysMetAlaLeuLeuLys 240
DB 661 AAACCTGGACAAAGCGCTGAAGAAGAAAGTGGCGAGAGATGGCTCTCTTGGAAAG 720
QY 241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
DB 721 GAAATCTTGGAGAAGGTGAGCAGCCCTTCACTGTGTCTCTGCGCTATGCTCTTGAAG 780
QY 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
DB 781 AAGACCCATCTCTGCTGTGATGAGCCCTGATGAATGGGGAGACCTCAAGTTCACATC 840
QY 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
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DB 841 TACAACGTGGGCACGCGTGGCTGGACATGACGCGGGTGATCTTTTACTCGGCCAGATA 900
QY 301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
DB 901 GCCTGTGGGATGCTGCACCTCCATGAACCTGGCATCGTCTATCGGGACATGAAGCCTGAG 960
QY 321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
DB 961 AATGTGCTTCTGGATGACCTCGGCACTGCGAGGTATCTGACCTGGGGCTGGCGTGGAG 1020
QY 341 MetLysGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
DB 1021 ATGAAGGTGGCAAGCCCATCACCAGAGGCTGGAACCAATGGTTATCATGGCTCCTGAG 1080
QY 361 IleLeuMetGluLysValSerTyrSerTyrProValAspTyrPheAlaMetGlyCysSer 380
DB 1081 ATCTTAATGGAAAGGTAAAGTTATTCCTATCTGTGAGCTGGTTTCCATGGGATGCAGC 1140
QY 381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
DB 1141 ATTTATGAATGGTTGTCTGGACGAACACCATTCAGAGATTACAAGGAAAGGTGAGTAA 1200
QY 401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPhThr 420
DB 1201 GAGGATCTGAAGCAAGAACTCTGCAAGACGAGGTCAAATTCAGCATGATTAACCTTACA 1260
QY 421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLysGly 440
DB 1261 GAGGAAGCAAAAGATATTTGCGAGCTCTTCTGGCTAAGAAACCCAGACCAAGCTTAGA 1320
QY 441 SerArgGluLysSerAspAspProArgLysHisHisPhePheLysThrIleAsnPhePro 460
DB 1321 AGCAGAGAAAGTCTGATGATCCCGAGGAACATCATTTCTTTAAACGATCAACTTCT 1380
QY 461 ArgLeuGluAlaGlyLeuIleGluProPheValProPheValProAspProSerValTyrAla 480
DB 1381 CGCCTGGAAGCTGGCTAAATTTGAACCCCACTTGTGCCAGACCCCTTCACTGGTTAT 1440
QY 481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
DB 1441 AAAGCATCGCTGAAATTTGATGATTTCTCGAGGTTGCGGGGGTGGAAATTTGATGACAA 1500
QY 501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGlu 520
DB 1501 GATAGCAGTTCTTCAAAACCTTTGCGACAGTGTCTGTCTATAGCATGCGAGGAGAA 1560
QY 521 IleIleGluThrGlyLeuPheGluLeuLeuAsnAspProAsnArgProThrGlyCysGlu 540
DB 1561 ATTATAGAAACGGGACTGTTTGGAGAACTGAATGACCCCAACAGACCTTACGGGTTG 1620
QY 541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
DB 1621 GAGGTAATTCATCAAGTCTGGCGTGTGTTGTTATTG 1659
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RESULT 2

US-10-044-205A-1
; Sequence 1. Application US/10044205A
; Publication No. US2002012346A1
; GENERAL INFORMATION:
; APPLICANT: KAPPELLER-LIBERMANN, Rosana
; APPLICANT: BANDARU, Rajasekhara
; TITLE OF INVENTION: 69087, 15821, and 15418, Methods and Compositions of Human Protein
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 10147-52U1
; CURRENT APPLICATION NUMBER: US/10/044, 205A
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/242,428
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: US 60/241,884
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/241,877
; PRIOR FILING DATE: 2000-10-20

; NUMBER OF SEQ ID NOS: 44
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 2198
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-044-205A-1

Alignment Scores:
 Pred. No.: 0 Length: 2198
 Score: 2889.00 Matches: 553
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 13 Gaps: 0

US-10-044-205A-2 (1-553) x US-10-044-205A-1 (1-2198)

Qy 1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
 Db 291 ATGGTGGACATGGGGGCGCTGGACAACTGATCGCAACACCGCTACCTGCGAGCGCGG 350
 Qy 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
 Db 351 AAGCCCTCGACTGCGACAGCAAGAGCTGCGAGCGCGCGCTAGCTGGCCCTGGCC 410
 Qy 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
 Db 411 GGGCTGACGGCTGGCGGAGCTCGCCAGAGCTGTCCCTGAACTTCCACAGCCCTGTGT 470
 Qy 61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
 Db 471 GAGCAGCAGCCCATCGCTCGCGCTCTTCGTGACTTCTAGCCACAGTGCACAGTTC 530
 Qy 81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluClyPro 100
 Db 531 CGCAAGCGGGCAACCTTCTAGAGACGTCGCAAACTGGAGCTGGCGAGGAGGAGCCC 590
 Qy 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
 Db 591 ACCAAGACAGCGCGCTGCGGGGCTGTGTGCGACTTGTGCGAGTGGCCCTGGCCCGGG 650
 Qy 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
 Db 651 AACCGCAACCTTCTCAGCGAGCGCTGGCCACCAAGTGCCAAAGCAGCAGCACCACCTG 710
 Qy 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
 Db 711 GAAGAGCAGTGGCTGCGAGTACGCTGCGCAAGGCTGAGGCCATGGCTTCTTTCGAAG 770
 Qy 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
 Db 771 CAGCCCTTTAGGATTTCTGACAGCGCTTCTACGACAGATTTCTGCGAGTGGAACTC 830
 Qy 181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
 Db 831 TTCGAGTGCACCAAGTGTACCAAGTACTTCTCACTGAGTTTCAGAGTGTGCGGGAAGGT 890
 Qy 201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
 Db 891 GGTTTTGGGAGGTATGTGCCCTCAGGTGAAACACCTGGGAAGATGTATGCTCCTGTAAG 950
 Qy 221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGlyLysMetAlaLeuLeuLys 240
 Db 951 AAATCTGGACAGACGGCTGAAGAGAAAGTGGCGAGAGATGGCTCTCTTGGAAAG 1010
 Qy 241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaThrAlaPheGluSer 260
 Db 1011 GAAATCTTGGAGAAGGTGAGCAGCCCTTTCATTGTCTCTCTGCTATGCTTTCAGAGC 1070
 Qy 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyLysAspLeuLysPheHisIle 280
 Db 1071 AAGACCCATCTCGCTTGTGATGAGCCTGATGAATGGGGAGAGCTCAAGTTCACATC 1130

Qy 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
 Db 1131 TACAACGTGGGCACGCGTGGCTGGACATGACCGGGTGATCTTTTACTCGGCCAGATA 1190
 Qy 301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
 Db 1191 GCCTGTGGGATGCTGCACCTCCATGAACCTCGGCATCGTCTATCGGGAGCATGAAGCTGAG 1250
 Qy 321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
 Db 1251 AATGTGCTTCTGGATGACCTCGCAACTGCAAGTTATCTGACCTGGGCTGGCCGTGGAG 1310
 Qy 341 MetLysGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
 Db 1311 ATGAAGGTGGCAAGCCCATCCACAGAGGCTGGACCAATGGTTACATGGCTCTCTGAG 1370
 Qy 361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
 Db 1371 ATCCTAATGGAAAGGTAAAGTTATTCCTATCTGTGGACTGGTTTGGCATGGGATGCAGC 1430
 Qy 381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
 Db 1431 ATTTATGAATGGTTGCTGGACGAACCATTCAAAGATTACAGAGAAAGGTCACTAAA 1490
 Qy 401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
 Db 1491 GAGGATCTGAAGCAAGAACTCTGCAAGCAGAGTCAAAATTCAGCATGATAACTTCACA 1550
 Qy 421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
 Db 1551 GAGGAAGCAAAAGATATTTGCGAGCTCTTCTGGCTAAGAAACCCAGAGCAACGCTTAGGA 1610
 Qy 441 SerArgGluLysSerAspAspProArgLysHisPhePheLysThrIleAsnPhePro 460
 Db 1611 AGCAGAGAAAGTCTGATGATCCCGAGAAACATCATTTCTTTAAACCATCACTTCTCT 1670
 Qy 461 ArgLeuGluAlaGlyLeuIleGluProPheProPheValProAspProSerValTyrAla 480
 Db 1671 CGCTGGAAGCTGGCTTAATTTGAACCCCAATTTGTGCCAGACCCCTTCAGTGGTTTATGCC 1730
 Qy 481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspLys 500
 Db 1731 AAAGACATCGCTGAAATTTGATGATTTCTCAGGTTTCGGGGGGTGGAAATTTGATGACAAA 1790
 Qy 501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGlu 520
 Db 1791 GATAGCAGTTCTTCAAAAACCTTTGCGACAGGTGCTGTCTCTATAGCATGGCAGGAGNA 1850
 Qy 521 IleIleGluThrGlyLeuPheGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
 Db 1851 ATTATAGAAACGGGACTGTTTGGAGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1910
 Qy 541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
 Db 1911 GAGGGTAATTCATCAAGTCTGGCGTGTGTTGTTATTG 1949

RESULT 3

US-09-802-117-1
 ; Sequence 1, Application US/09802117
 ; Publication No. US20020042503A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Walke, D. Wade
 ; APPLICANT: Wilganowski, Nathaniel L.
 ; APPLICANT: Turner, C. Alexander Jr.
 ; TITLE OF INVENTION: No. 644456el Human G-Coupled Protein Receptor Kinases and Polym
 ; FILE REFERENCE: LEX-0147-USA
 ; CURRENT APPLICATION NUMBER: US/09/802,117
 ; CURRENT FILING DATE: 2001-03-08
 ; PRIOR APPLICATION NUMBER: US 60/188,449
 ; PRIOR FILING DATE: 2000-03-10
 ; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 1662
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 ; US-09-802-117-1

Alignment Scores:

Pred. No.: 0 Length: 1662
 Score: 2883.00 Matches: 552
 Percent Similarity: 99.82% Conservative: 0
 Best Local Similarity: 99.82% Mismatches: 1
 Query Match: 99.79% Indels: 0
 DB: 9 Gaps: 0

US-10-044-205a-2 (1-553) x US-09-802-117-1 (1-1662)

Qy 1 MetValAspMetGlyAlaLeuAspAsnLeuLeuAlaAsnThrAlaTyrLeuGlnAlaArg 20
 Db 1 ATGGTGGACATGGGGCCCTGGAYAACTGATCGCCAAACACCGCTACCTGCAGGCCGG 60
 Qy 21 LysProSerAspCysAspSerLysGlnLeuGlnArgArgArgSerLeuAlaLeuPro 40
 Db 61 AAGCCCTCGACTGGGACAGCAAGAGCTGCAGCGCGCGCGCTAGCCTGGCCCTGCC 120
 Qy 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
 Db 121 GGCGTGCAGGGTGGCGGAGCTCGCCAGAACCTGTCCCTGAACTTCCACAGCCTGHT 180
 Qy 61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
 Db 181 GAGCAGCAGCCCATCGGTCCGCGCTCTTCGTGACTTCTTAGCCACAGTGCACAGTTC 240
 Qy 81 ArgLysAlaAlaThrPheLeuGlnAspValGlnAsnTrpGluLeuAlaGluGlyPro 100
 Db 241 CGCAAGGGCGCAACCTTCCTAGAGACGTCGCAAACTGGGAGCTGGCGAGGAGGACCC 300
 Qy 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
 Db 301 ACCAAGACAGCGCGCTCAGGGGCTGGTGCCACTTGTGGAGTGCCTTGCCTGCCCGGG 360
 Qy 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
 Db 361 AACCCGCAACCTTCTCAGCCAGCGCTGGCCACCAAGTGCACAGCAGCCACTGAG 420
 Qy 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
 Db 421 GAAGAGCGAGTGGCTGCAGTACGCTGGCCAGGCTGAGGCCATGGCTTCTTGCAGAG 480
 Qy 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
 Db 481 CAGCCCTTTAGGATTTGTGACACAGCGCTTCTAGACAAAGTTTCTGCAGTGGAAATC 540
 Qy 181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
 Db 541 TTCGAGATGCACCAAGTTCAGACAAGTACTTCACTGATTCAGAGTTCGCGGAAAGGT 600
 Qy 201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
 Db 601 GGTTTTGGGAGGTATGTGCGCTCCAGGTGAAAAACACTGGGAAGATGATGCTCTGAAG 660
 Qy 221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuGluLys 240
 Db 661 AAATCGACAGAGCGCTGAGAAAGAGGTGGCGAGAGATGGCTCTCTTGGAAAG 720
 Qy 241 GluLeuGluLysValSerSerProPheLeuValSerLeuAlaTyrAlaPheGluSer 260
 Db 721 GAAATCTTGGGAAGGTGAGAGCCCTTCTATGTCTCTCTGGCCCTATGCTCTTGGAGC 780
 Qy 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLysPheHisIle 280
 Db 781 AAGACCCATCTCTGCTTGTATGAGCCTGATGAATGGGGAGAGCCTCAAGTTCACATC 840

Qy 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
 Db 841 TACAACGTGGGACGCGTGGCTGGACATGAGCGGGTGATCTTTTACTTCGGCCAGATA 900
 Qy 301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
 Db 901 GCCTGTGGATGCTGCACCTCATGAACTCGGCATCGTCTATCGGACATGAAGCTGAG 960
 Qy 321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
 Db 961 AATGTGCTTCGGATGACCTCGCAACTGCAAGGTATATCGACCTGGGCTGGCCCTGGAG 1020
 Qy 341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
 Db 1021 ATGAAGGTGGCAAGCCCATCCACAGAGGCTGGACCAATGGTTACATGGCTCTGAG 1080
 Qy 361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
 Db 1081 ATCCTAATGAAAAAGGTAAGTTATTCCTATCCTGTGGAAGTGGTTGCCATGGATGCAGC 1140
 Qy 381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
 Db 1141 ATTTATGAAATGGTGTGTCGACGAACACCATTCAAAGATTACAAGGAAAAAGGTCAGTAA 1200
 Qy 401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
 Db 1201 GAGGATCTGAAGCAAGAACTCTGCAGACAGAGTCAANTTCCAGCATGATACTTACA 1260
 Qy 421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
 Db 1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAAGCAACGCTTAGGA 1320
 Qy 441 SerArgGluLysSerAspAspProArgLysHisPhePheLysThrIleAsnPhePro 460
 Db 1321 AGCAGAGAAAGTCTGATGATCCAGGAAACATCATTTCTTTAAACCATCAACTTCTC 1380
 Qy 461 ArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValTyrAla 480
 Db 1381 CGCTCGAAGCTGGCTTAATTTGAACCCCATTTGTGCCAGACCTTTCAGTGGTTATGCC 1440
 Qy 481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
 Db 1441 AAAGACATCGCTGAAATGATGATTTCTCTGAGGTTCGGGGGGTGGAAATTTGATGACAAA 1500
 Qy 501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu 520
 Db 1501 GATAAGCAGTTCTTTCAAAACCTTTTGCAGACAGTGTCTTCTATAGCATGCGAGGAGAA 1560
 Qy 521 IleIleGluThrGlyLeuPheGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
 Db 1561 ATTATAGAACGGGACTGTTTGAGGAACCTGAATGACCCCAACACACCTACGGTTGTGAG 1620
 Qy 541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
 Db 1621 GAGGTAATTCATCAAGTCTGGCGTGTGTTGTTATTG 1659

RESULT 4

US-10-217-745-1
 ; Sequence 1, Application US/10217745
 ; Publication No. US20030004328A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wilganowski, Nathaniel L.
 ; APPLICANT: Turner, C. Alexander Jr.
 ; TITLE OF INVENTION: No. US20030004328A1
 ; TITLE OF INVENTION: Polynucleotides
 ; FILE OF INVENTION: Encoding the Same
 ; FILE REFERENCE: LEX-0147-USA
 ; CURRENT APPLICATION NUMBER: US/10/217,745
 ; CURRENT FILING DATE: 2002-08-12
 ; PRIOR APPLICATION NUMBER: US/09/802,117
 ; PRIOR FILING DATE: 2001-03-08
 ; NUMBER OF SEQ ID NOS: 5

Human G-Coupled Protein Receptor Kinases an

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1

LENGTH: 1662

TYPE: DNA

ORGANISM: homo sapiens

US-10-217-745-1

Alignment Scores:

Pred. No.:	0	Length:	1662
Score:	2883.00	Matches:	552
Percent Similarity:	99.82%	Conservative:	0
Best Local Similarity:	99.82%	Mismatches:	1
Query Match:	99.73%	Indels:	0
DB:	14	Gaps:	0

US-10-044-205A-2 (1-553) x US-10-217-745-1 (1-1662)

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Qy 1 MetValAspMetGlyAlaLeuAspMetLeuLeuAlaAenThrAlaTyrLeuGlnAlaArg 20
Db 1 ATGGTGGACATGGGGGCGCTGGAYAACCTGATCGGCAACACCGCTACCTGCAGGCCCGG 60

Qy 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgSerLeuAlaLeuPro 40
Db 61 AAGCCCTCGGACTGCGACAGCAAGAGCTGCAGCGCGCGCGCTAGCCTGGCCCTGCC 120

Qy 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
Db 121 GGGCTGCAGGGCTGGCGGAGCTCGCCAGAGCTGCTCCGAACTTCCACAGCCCTGTGT 180

Qy 61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
Db 181 GAGCAGCAGCCCATCGGTGGCGCTCTTCGCTGACTTCCTAGCCACAGTGCACCGTTC 240

Qy 81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGlyPro 100
Db 241 CGCAAGCGGGCAACCTTCTAGAGAGCTGCAGAACTGGAGCTGGCGAGGAGGAGGCC 300

Qy 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
Db 301 ACCAAAGACAGCGCTCGAGGGCTGGTGGCCACTTGTGGAGTGGCCCTGCCCGCGGG 360

Qy 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
Db 361 AACCGCAACCTTCTCAGCAGCGCTGGCCACCAAGAGTGCACAGCAGCCACCACTGAG 420

Qy 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
Db 421 GAAGAGCAGTGGCTGCAGTACGCTGGCCAGGCTGAGGCCATGGCTTCTTTCAGAG 480

Qy 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
Db 481 CAGCCCTTTAAGGATTTCTGTACACAGCGCTTCTACGACAAAGTTTCTGCAGTGGAAAGCTC 540

Qy 181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
Db 541 TTCGAGATGCACCAAGTGTACAGCAAGTACTTCACTGAGTTTCAGAGTGTCTGGGAAAGGT 600

Qy 201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
Db 601 GTTTTGGGAGGTATGTGCCCTCAGGTGAAACACTGGGAAGATGTATGCCCTGTATAG 660

Qy 221 LysLeuAspLysLysArgLeuLysLysGlyGlyGlyLysMetAlaLeuLeuGluLys 240
Db 661 AAACCTGCACAGACCGCTGAAGAAGAAAGTGGCGAGAGAGTGGCTCTCTTGGAAAG 720

Qy 241 GluLeuLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
Db 721 GAAATCTTGGAGAGGTGAGCAGCCCTTTCAATGTCTCTGGCCCTATGCTCTTTCAGAGC 780

Qy 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
Db 781 AAGACCCATCTCTGCTTGTATGAGCCTGATGAATGGGGAGAGCCTCAAGTTCACATC 840

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Qy 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
Db 841 TACAACGTGGCAGCGCTGGCATGAGCCGGGTATCTTTTACTCGGCCCCAGATA 900

Qy 301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
Db 901 GCCTGTGGAGTGTGCACCTCATGNACTCGGCATCGTCTATCGGGACATGAGGCTGAG 960

Qy 321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
Db 961 AATGTGCTTCTGGATGACCTCGCAACTGCAGGTTATCTGACCTGGGCTGGCGTGGAG 1020

Qy 341 MetLysGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
Db 1021 ATGAAGGTGGCAAGCCCATCACCCAGAGGCTGGAACCAATGGTTACATGCTCTCTGAG 1080

Qy 361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
Db 1081 ATCTTAATGGAAAGGTAAAGTTATCTCTGTGGACTGGTTTGGCATGGGATGCAGC 1140

Qy 381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
Db 1141 ATTTATGAATGGTTGTCTGGACCAACCACTTCAAGAGATTACAAGAAAGGTCAGTAAA 1200

Qy 401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
Db 1201 GAGGATCTGAAGCAAGAACTCTGCAAGCAGAGTCAAAATTCACAGCATGATAACTTCACA 1260

Qy 421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
Db 1261 GAGGAAGCAAAAGATATTGTGAGGCTTCTTGGCTAAGAAACCAAGAGCAAGCTTAGGA 1320

Qy 441 SerArgGluLysSerAspAspProArgLysHisPhePheLysThrIleAsnPhePro 460
Db 1321 AGCAGAGAAAGTCTGATGATCCCGAGGAAACATCATTTCTTTAAACCATCAACTTCT 1380

Qy 461 ArgLeuGluAlaGlyLeuIleGluProPhePheValProAspProSerValValTyrAla 480
Db 1381 CGCCTGGAAGCTGGCTAAATTTGAACCCCACTTTGTGCCAGACCCCTTCAGTGGTTTATGCC 1440

Qy 481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
Db 1441 AAAGACATCGCTGAAATTTGATGATTTCTGAGGTTTCGGGGGTGGAAATTTGATGACAAA 1500

Qy 501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGlu 520
Db 1501 GATAAGCAGTTCTTCAAAACCTTTGGCAGACGCTGCTGTCTCTATAGCATGGCAGAGAA 1560

Qy 521 IleIleGluThrGlyLeuPheGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
Db 1561 ATTATAGAAACGGGACTGTTTGGAGNACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy 541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
Db 1621 GAGGTAATTCATCAAGTCTGGCGTGTGTTGTTATTG 1659

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RESULT 5

US-10-311-034-45
 ; Sequence 45, Application US/103111034
 ; Publication No. US20040023242A1
 ; GENERAL INFORMATION:
 ; APPLICANT: INCYTE GENOMICS, INC.
 ; APPLICANT: YUE, Henry
 ; APPLICANT: LAL, Preeti
 ; APPLICANT: BANDMAN, Olga
 ; APPLICANT: BOROMSKI, Mark L.
 ; APPLICANT: AU-YOUNG, Janice
 ; APPLICANT: LU, Yan
 ; APPLICANT: GANDHI, Ameena R.
 ; APPLICANT: TRIBOULEY, Catherine M.
 ; APPLICANT: CHAWLA, Narinder K.
 ; APPLICANT: YAO, Monique G.
 ; APPLICANT: LU, Dyung Aina M.

```

; APPLICANT: GREENWALD, Sara R.
; APPLICANT: RAMKUMAR, Jayalaxmi
; APPLICANT: GRIFFIN, Jennifer A.
; APPLICANT: KEARNEY, Liam
; APPLICANT: BURFORD, Neil
; APPLICANT: NGUYEN, Damiel B.
; APPLICANT: TANG, Y. Tom
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: HE, Ann
; APPLICANT: THORNTON, Michael
; APPLICANT: HAPALIA, April
; APPLICANT: ARVIZU, Chandra S.
; APPLICANT: GURURAJAN, Rajagopal
; APPLICANT: LO, Terence P.
; APPLICANT: KHAH, Farrah A.
; APPLICANT: RECIPON, Shirley A.
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: POLICKY, Jennifer L.
; APPLICANT: DING, Li
; APPLICANT: GREYER, Megan
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: THANGAVELU, Kavitha
; APPLICANT: BATRA, Sajeev
; APPLICANT: ISON, Craig H.
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0125 PCT
; CURRENT APPLICATION NUMBER: US/10/311,034
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372;
; 60/228,056
; PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-07-25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PERL Program
; SEQ ID NO 45
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040023242A1 7477204CB1
US-10-311-034-45

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Alignment Scores:

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Pred. No.: 0 Length: 1662
Score: 2883.00 Matches: 552
Percent Similarity: 99.82% Conservative: 0
Best Local Similarity: 99.82% Mismatches: 1
Query Match: 99.79% Indels: 0
DB: 17 Gaps: 0

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US-10-044-205A-2 (1-553) x US-10-311-034-45 (1-1662)

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Qy 1 MetValAspMetGlyAlaLeuAspSerLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
Db 1 ATGTGGACATGGGGCCCTGGACAACTGATCGCCAAACACCGCCCTACCTGCGAGCCGG 60
Qy 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgArgArgArgArg 40
Db 61 AAGCCCTCGGACTGGACAGCAAGAGCTGCGAGCGCGCGGCTAGCTGGCCCTGCC 120
Qy 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
Db 121 GGGCTGCGAGGCTGCGCGAGCTCGCCAGAGAGCTGCCGAACTTCCACAGCCCTGTGT 180
Qy 61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
Db 181 GAGCAGCAGCCCATCGGTGCGCGCTCTTCGTGACTTCTAGCCACAGTGGCCACGTTTC 240
Qy 81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGlyPro 100
Db 241 CGCAAGCGCGCAACCTTCTAGAGGACGTGCAAGAACTGGAGCTGGCCGAGGGAGCCC 300

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Qy 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
Db ACCAAGACACGCGCTGCGAGGGCTGCTGCCCACTTGTGCGAGTGCCTTGCCTGCGCGGG 360
Qy 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
Db AACCGCAACCTTCTCTCAGCCAGCGCTGCCCACTCAAGAGTCCCAAGCAGCCACCACTGAG 420
Qy 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
Db GAAGAGCGAGTGGCTGCGAGTGCAGCTGCCAAGCTGAGCCATGGCTTCTTTCGACAGAG 480
Qy 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
Db CAGCCCTTTAAGGATTTCTGTCAGCCAGCGCTTCTACGACAAAGTTTCTCAGTGGAAATCTC 540
Qy 181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
Db TTCGAGATGCAACCACTGTCAGACAAGTACTTCACTGAGTTTCAGAGTCTCTGGGAAAGGT 600
Qy 201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
Db GGTTCGCGAGGATATGTCGCTCAGGTGAACACTGGAGAGATGATGCTCTGTAAAG 660
Qy 221 LysLeuAspLysLysArgLeuLysLysGlyGlyGlyLysMetAlaLeuLeuGluLys 240
Db AAACCTGGCAAGAGCGCTGCAAGAAAGAGTGGCGAGAGATGGCTCTCTTGGAAAG 720
Qy 241 GluLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
Db GAATCTTTGGAGAGGTGAGCAGCGCTTCACTTGTCTCTCTGGCTTATGCTCTTGGAGAGC 780
Qy 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisLe 280
Db AAGACCACTCTCTGCTTGTCTGATGAGCTGATGAGTGGGGAGAGCTCAAGTTCCACATC 840
Qy 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
Db TACAACGTGGGCACGCGTGGCTGACATGACCGGGTGATCTTTTACTCGGCCAGATA 900
Qy 301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
Db GCCTGTGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960
Qy 321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
Db AATGTGCTTCTGGATGACCTCGCACTCGAGGTATCTGACCTGGGGCTGGCGGTGGAG 1020
Qy 341 MetLysGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
Db ATGAAGGTGGCAAGCCCATCACCAGAGGCTGGAAACCAATGGTTACATGGCTCCTGAG 1080
Qy 361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
Db ATCTTAATGGAAAGGTAAAGTTATTCCTTCTCTGGAAGTGTTCCTCATGGGATGCGAGC 1140
Qy 381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
Db ATTTATGAAATGGTGTGTCGACGACCACTTCAAGATTTACAGAGAAAGGTGAGTAAA 1200
Qy 401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
Db GAGGATCTGAAGCAAGAACTCTCAAGACGAGGTCAAAATTCAGAGCATGATAACTTACA 1260
Qy 421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
Db GAGGAAGCAAAAGATATTTGAGGCTCTTCTGCTGCTTGAAGAAACAGAGCAACGCTTAGGA 1320
Qy 441 SerArgGluLysSerAspProArgLysHisPhePheLysThrIleAsnPhePro 460
Db AGCAGAGAAAGTCTGATGATCCAGGAGAAACATCATTTCTTTAAACGATCAACTTCTCT 1380
Qy 461 ArgLeuGluAlaGlyLeuIleGluProPheValProAspProSerValTyrAla 480

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Db 1381 CCCCCTGGAGCTGGCTTAATTAACCCCATTTGTGCCAGACCCCTTCAGTGGTTTATGCC 1440
Qy 481 LysAspIleAlaGluLeuAspPheSerGluValArgGlyValClnPheAspPheLys 500
Db 1441 AAAGACATCGCTGAATGATGATTTCTGAGGTTGGGGGGTGGATTTGATGACAAA 1500
Qy 501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaThrGlnGluGlu 520
Db 1501 GATAAGCAGTTCTTCAAAACATTTTCGACAGGTGCTGTTCTTATAGCATGGCAGGAAGA 1560
Qy 521 IleIleGluThrGlyLeuPheGluClnLeuAsnAspProAsnArgProThrGlyCysGlu 540
Db 1561 ATTATAGAAACGGGACTGTTTGAGGAACCTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
Qy 541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
Db 1621 GAGGGAATTCATCCAGCTGGCGTGTGTTGTTATTG 1659

RESULT 6

US-10-451-168-49
; Sequence 49, Application US/10451168
; Publication No. US20040091969A1
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM P.L.C.
; APPLICANT: GLAXO GROUP LIMITED
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50039
; CURRENT APPLICATION NUMBER: US/10/451,168
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/US01/49232
; PRIOR FILING DATE: 2000-12-17
; PRIOR APPLICATION NUMBER: 60/256,710
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/257,048
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/260,482
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/264,922
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/266,797
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/276,988
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/281,535
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/289,622
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-451-168-49

Alignment Scores:
Pred. No.: 0 Length: 1662
Score: 2883.00 Matches: 552
Percent Similarity: 99.82% Conservatives: 0
Best Local Similarity: 99.82% Mismatches: 1
Query Match: 99.79% Indels: 0
DB: 17 Gaps: 0

US-10-044-205A-2 (1-553) x US-10-451-168-49 (1-1662)

Qy 1 MetValAspMetGlyValLeuAspPheLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
Db 1 ATGGTGGACATCGGGGCCCTTGACCAACCTGATCGCCACACCGCTACCTCGAGGCCCGG 60
Qy 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgSerLeuAlaLeuPro 40

Db 61 AAGCCCTCGAAGCTGGACAGCAAGAGCTGCAGCGGCGCGCTAGCTGGCCCTGCCCC 120
Qy 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
Db 121 GGGCTGCAGGCTGCGCGAGCTCGCCAGAAAGCTGTCCCTGAACTTCCACAGCCCTGTGT 180
Qy 61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
Db 181 GAGCAGCAGCCATCGGTCGCGGCTCTTCCGTGACTTCTTAGCCACAGTGGCCACGTTTC 240
Qy 81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
Db 241 CGCAAGGCGGCACTTCTTAGAGAGCTGCAGAACTGGGAGCTGGCGAGGAGGGACCC 300
Qy 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
Db 301 ACCAAAGACAGCGGCTGCAGGGCTGGTGCCACTTGTGCGAGTGCCTGCCCCCGGG 360
Qy 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
Db 361 AACCGCGCAACCTTCTCAGCAGCGCGTGCCCAAGTAGTCCCAAGCAGCCACCACTGAG 420
Qy 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
Db 421 GAAGAGCGAGTGGCTGCGAGTGACGCTGCCAAGGCTGAGGCCATGGCTTTCTTGCAAG 480
Qy 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
Db 481 CAGCCCTTTAAGGATTTGCTGACCGAGCGCTTCTACGACAAAGTTTCTGCAGTGGAACTC 540
Qy 181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
Db 541 TTCGAGATGCAACCAAGTGTTCAGACAAGTACTTCACTGAGTTTCAGAGTCTCTGGGAAAG 600
Qy 201 GlyPheGlyGluValCysAlaValGlnValLysValThrGlyLysMetTyrAlaCysLys 220
Db 601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAACACTGGGAAGATGATGCTCTGTAG 660
Qy 221 LysLeuAspLysLysArgLeuLysLysGlyGlyGluLysMetAlaLeuLeuLys 240
Db 661 AAACCTGGACAGAGCGGCTGACAGAAAGAGTGGCGAGAGATGGCTCTCTTGGAAAG 720
Qy 241 GluLeuLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
Db 721 GAAATCTTTGGAGAAGGTTCAGCAGCGCTTTCATTTGTCTCTGCGCTATGCTCTTGAG 780
Qy 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
Db 781 AAGACCCCATCTCTGCTTGTCTATGAGCCTGATGATGGGGGAGAGCTCAAGTTCCACATC 840
Qy 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
Db 841 TACAACGTGGGCACCGGTGGCTGGACATGAGCGGGTGATCTTTTACTCGGCCCAGATA 900
Qy 301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
Db 901 GCCTGTGGATGCTGCACCTCCATCAACTCGCATCGTCTATCGGGACATGAAGCTCGAG 960
Qy 321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
Db 961 AATGTGCTTCTGGATGACCTCGCAACTGCGAGGTATCTGACCTGGGGCTGGCCGTGGAG 1020
Qy 341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
Db 1021 ATGAAGGTGGCAAGCCCATCACCCAGAGGGCTGGAAACCAATGGTTACATGGCTCCTG 1080
Qy 361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
Db 1081 ATCTTAATGGAAGTAAGTTATTCCTATCTCTGTGGACTGGTTTGCATGGGATGCAGC 1140
Qy 381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
Db 1141 ATTTATGAATGGTGTGGTGGACGAACACCATTCAAAGATTACAGGAAAGAGTTCAGTAAA 1200

QY 401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
DB 1201 GAGGATCTGAACCAAGAACTCTGCAAGACGAGGTCAATTTCCAGCATGATAACTTCACA 1260
QY 421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
DB 1261 GAGGAAGCAAAAGATATTTCAGGCTCTCTTGGCTAAGAAACCAAGAGCAACGCTTAGGA 1320
QY 441 SerArgGluLysSerAspAspProArgLysHisPhePheLysThrIleAsnPhePro 460
DB 1321 AGCAGAGAAAGCTGATGATCCCAAGGAAACATCAATTTCTTAAACCATCAACTTTCTCT 1380
QY 461 ArgLeuGluAlaGlyLeuIleGluProPheValProAspProSerValValTrAla 480
DB 1381 CGCTGGGAAGCTGGCTTAATGAACCCCAATTTGTGCCAGACCTTCAGTGGTTATGCC 1440
QY 481 LysAspIleAlaGluLysAspPheSerGluValArgGlyValGluPheAspAspLys 500
DB 1441 AAAGACATCGCTGAATTTGATGATTTCTGAGGTTCCGGGGGTGGAATTTGATGACAAA 1500
QY 501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaThrGlnGluGlu 520
DB 1501 GATAAGCAGTTCTTCAAAACATTTTGGACAGGTGCTGTCTTATAGCATGGCAGGAAGA 1560
QY 521 IleIleGluThrGlyLeuPheGluLeuLeuAsnAspProAsnArgProThrGlyCysGlu 540
DB 1561 ATTATAGAAACGGGACTGTTGAGGAACTGAATGACCCCAACAGACCTACGGGTGTGAG 1620
QY 541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
DB 1621 GAGGCTAATTCATCAAGTCTGGCGTGTGTTGTTATTG 1659

RESULT 7

US-10-788-197-22
; Sequence 22, Application US/10788197
; Publication No. US20050032125A1
; GENERAL INFORMATION:
; APPLICANT: OAKLEY, ROBERT H.
; APPLICANT: HUDSON, CHRISTINE C.
; TITLE OF INVENTION: CONSTITUTIVELY TRANSLOCATING CELL LINE
; FILE REFERENCE: NRK.108
; CURRENT APPLICATION NUMBER: US/10/788,197
; PRIOR FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: PCT/US03/14581
; PRIOR FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: 60/379,986
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: 60/401,698
; PRIOR FILING DATE: 2002-08-07
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 22
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-788-197-22

Alignment Scores:
Pred. No.: 0 Length: 1662
Score: 2883.00 Matches: 552
Percent Similarity: 99.82% Conservative: 0
Best Local Similarity: 99.82% Mismatches: 1
Query Match: 99.79% Indels: 0
DB: 19 Gaps: 0

US-10-044-205A-2 (1-553) x US-10-788-197-22 (1-1662)

QY 1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyLeuGlnAlaArg 20
DB 1 ATGGTGGACATGGGGGGCCCTGACAACTGATCGCAACACCGCCCTACTGAGGCCCGG 60
QY 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgSerLeuAlaLeuPro 40

DB 61 AAGCCCTCGGACTCGCAGCAAGAGCTGCAGCGCGCGCTAGCCTGGCCCTGCCC 120
QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAenPheHisLeuLeuCys 60
DB 121 GGGCTGAGGGCTCGCGGAGCTCCGCAGAAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
QY 61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
DB 181 GAGCAGCAGCCCATCGCTGCGCGCTCTTCGTGACTTCTTAGCCACAGTGCACCGTTC 240
QY 81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
DB 241 CGCAAGCGCGCAACCTTCTTAGAGACGTGCAGAACTGGGAGCTGGCGAGGAGGAGCCC 300
QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
DB 301 ACCAAAGACAGCGCGCTGCAGGGCTGTGTGCCACTTGTGTGAGTGTGCCCTGCCCCGGG 360
QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
DB 361 AACCCGCAACCTTCTTAGCCAGCGCTGGCCACCAAGTGCACAGCAGCCACCATGAG 420
QY 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
DB 421 GAAGAGCAGTGGCTGAGTGCAGTGCAGCTGCCAAGCTGAGGCTATGGCTTCTTGCAGAG 480
QY 161 GlnProPheLysAspPheValThrSerAlaPheTyraPheLysPheLeuGlnTrpLysLeu 180
DB 481 CAGCCCTTTAAGGATTTCTGACACCGCCCTTCTACGACAAAGTTCGTGAGTGTGAAACTC 540
QY 181 PheGluMetGlnProValSerAspLysTyraPheThrGluPheArgValLeuGlyLysGly 200
DB 541 TTCAGATGCAACCAAGTGTGCAGCAAGTACTTCACTGAGTTCAGAGTGTGGGGAAGGT 600
QY 201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyraLysCysLys 220
DB 601 GGTTCGGGAGGTATGTGCGCTCAGGTGAAAAACACTGGGAAGATGTATGCTGTAAAG 660
QY 221 LysLeuAspLysArgLeuLysLysGlyGlyGlyLysMetAlaLeuLeuGluLys 240
DB 661 AAATCGACAAAGACGGCTGAAGAAAGGTGGCAGAAAGATGGCTCTCTTGGAAAG 720
QY 241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyraLysPheGluSer 260
DB 721 GAATCTTGGGAAGGTTCAGCAGCCCTTCACTGCTCTGCGCTATGCTTGTGAGAGC 780
QY 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
DB 781 AAGACCATCTCTGCTTGTGCATGAGCTGATGAATGGGGAGACCTCAAGTTCACATC 840
QY 281 TyraAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyraSerAlaGlnIle 300
DB 841 TACAACGTGGGCACGCGCTGCATGACATGAGCGGGGTGATCTTTTATCTCGGCCAGATA 900
QY 301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyraArgAspMetLysProGlu 320
DB 901 GCCTGTGGATGTGACCTCCATGAACTGGCATCGTCTATCGGGACATGAAGCCTGAG 960
QY 321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
DB 961 AATGTGCTCTGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCGGTGAG 1020
QY 341 MetLysGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyraMetAlaProGlu 360
DB 1021 ATGAAGGTGGCAAGCCCATCACCCAGGGCTGGAACCAATGTTATCATGGCTCCTGAG 1080
QY 361 IleLeuMetGluLysValSerTyraProValAspTrpPheAlaMetGlyCysSer 380
DB 1081 ATCTATATGNAAGGTAGTATTCTCTCTGACCTGTTGCTGCTGCTGCTGCTGCTGCTG 1140
QY 381 IleTyraGluMetValAlaGlyArgThrProPheLysAspTyraLysGluLysValSerLys 400


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Db      1141 ATTTATGAATGGTTCTGGACCAACACCATTCATCAAGATTACAGGAAAAAGTCTAGTAAA 1200
Qy      401  GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
Db      1201 GAGGATCTGAAGCAAGAAGAACTCTGCAAGACGAGGTCAAAATTCACAGCATGATAACTTTCACA 1260
Qy      421  GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysPheGlnArgLeuGly 440
Db      1261 GAGGAAGCAAAAGATATTTCGAGGCTCTCTTGGCTAAGAAACCAAGACCAAGCTTAGGA 1320
Qy      441  SerArgGluLysSerAspAspProArgLysHisPhePheLysThrIleAsnPhePro 460
Db      1321 AGCAGAGAAAGTCTGATGATCCCAAGAAACATCATTTCTTTAAACGATCAACTTTCT 1380
Qy      461  ArgLeuGluAlaGlyLeuIleGluProPheValProAspProSerValValTrAla 480
Db      1381 CGCTGGAAGCTGGCTAATTGAACCCCAATTTGTGCCAGACCCCTTCAGTGGTTTATGCC 1440
Qy      481  LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
Db      1441 AAAGACATCGCTGAATATTGATGATTTCTGAGGTTTCGGGGGTGGAATTTGATGACAAA 1500
Qy      501  AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaThrGlnGluGlu 520
Db      1501 GATAGCAGTCTCTTCAAAACTTTTCGACAGGTGCTGTCTCTATAGCATGGCAGGAAGAA 1560
Qy      521  IleIleGluThrGlyLeuPheGluLeuLeuAsnAspProAsnArgProThrGlyCysGlu 540
Db      1561 ATTATAGAAACGGACTCTTTGAGGAACTGAATGACCCCAACAGACCTACGGTTGTGAG 1620
Qy      541  GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
Db      1621 GAGGTAAATCATCCAGTCTGGCGTGTGTGTTGTTATTG 1659

RESULT 8
US-09-802-117-5
; Sequence 5, Application US/09802117
; Publication No. US20020042503A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 64445661 Human G-Coupled Protein Receptor Kinases and Polym
; FILE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/09/802,117
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/188,449
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2249
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-802-117-5

Alignment Scores:
Pred. No.: 0 Length: 2249
Score: 2883.00 Matches: 552
Percent Similarity: 99.82% Conservative: 0
Best Local Similarity: 99.82% Mismatches: 1
Query Match: 99.79% Indels: 0
DB: 9 Gaps: 0

US-10-044-205A-2 (1-553) x US-09-802-117-5 (1-2249)
Qy      1  MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
Db      354 ATGGTGGACATGGGGGCGCTGGACAACTGATCGCCAAACACCGCTACTCGACGCCCGG 413
Qy      21  LysProSerAspCysAspSerLysGluLeuGlnArgArgArgSerLeuAlaLeuPro 40

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Db      414 AAGCCCTCGAAGCTGGACAGCAAGAGAGCTGCAGCGCGCGCGGTAGCTGGCCCTGCCCC 473
Qy      41  GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
Db      474 GGGCTGCAGGGCTGCGGGAGCTCCGCCAGAAAGCTGTCCCTGNACTTCCACAGCCTGTGT 533
Qy      61  GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
Db      534 GAGCAGCAGCCCATCGGTGCGCGCTCTTCCTGCTGACTTCTTAGCCACACAGTGGCCACGTTTC 593
Qy      81  ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGlnGlyPro 100
Db      594 CGCAGGCGGCAACCTTCTTAGAGACGTGCAGAACTGGAGCTGGCCAGGAGGAGACCC 653
Qy      101  ThrLysAspSerAlaLeuGlnGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
Db      654 ACCAAAGACAGCGCTGCAGGGCTGGTGCCACTTGTGCGAGTGCCTGCCCCCGGG 713
Qy      121  AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
Db      714 AACCGCAACCTTCTTCAGCAGCGCGCTGCACCAAGTGCACAAAGTGCACAGCCACCACTGAG 773
Qy      141  GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
Db      774 GAAGAGCAGTGGCTGCAGTGCAGCTGGCCAGGCTGAGGCCATGGCTTTCTTTCAGAG 833
Qy      161  GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
Db      834 CAGCCCTTTAAGGATTTCTGCACCGCGCTTCTACGACAAAGTTTCTGCAGTGGAACTC 893
Qy      181  PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
Db      894 TTCGAGATGCAACCAAGTGTGCAGCAAGTACTTCTACTGAGTTTCAGAGTGTGGGGAAGGT 953
Qy      201  GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
Db      954 GGTTTTGGGAGGTATGTGCCGTCCAGGTGAAAACACTGGGAAAGATGTATGCCCTGTAG 1013
Qy      221  LysLeuAspLysLysArgLeuLysLysGlyGlyGlyLysMetAlaLeuLeuGlyLys 240
Db      1014 AAACCTGGACAGAGCGGCTGACAGAGAAAGGTGGGAGAGAGATGGCTCTCTTGGAAAG 1073
Qy      241  GluLeuGluLysValSerSerPheIleValSerLeuAlaTyrAlaPheGluSer 260
Db      1074 GAAATCTTGGAGAAAGTCCAGCAGCCCTTCTATGTCTCTCTGGCTATGCTTTCAGAGC 1133
Qy      261  LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
Db      1134 AAGACCCCATCTCTGCTTGTCTATGAGCTGTATGAATGGGGAGAGACCTCAAGTTCCACATC 1193
Qy      281  TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
Db      1194 TACAACGTGGGACAGCGGTGGCTGGACATGAGCGGGTGTATCTTTACTCGGCCAGATA 1253
Qy      301  AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
Db      1254 GCCTGTGGATGTCTGCACCTCCATGAACCTCGGCATCGTCTATCGGAGACATGAAGCTCGAG 1313
Qy      321  AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
Db      1314 AATGTGCTTCTGGATGACCTCGGCAACTGCAAGTTATCTGACCTGGGGCTGGCCCTGGAG 1373
Qy      341  MetLysGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
Db      1374 ATGAAGGTGGCAAGCCCATCCACAGAGGCTGGAACCAATGGTTACATGGCTCTGTAG 1433
Qy      361  IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
Db      1434 ATCTAATGGAAGAAAGTAAGTTATTCCTATCTCTGTGGAGTGGTTTGGCCATGGGATGCAGC 1493
Qy      381  IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
Db      1494 ATTTATGAATGGTTGCTGGAGCAACCACTTCAAGAGATTACAAGGAAAAAGGTTCAGTAAA 1553

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QY 401 GluAspLeuValGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
DB 1554 GAGGATCTGAGCAAGAAAGAACTCTGCAAGACGAGGTCAAAATTCACGATGATAACTTCACA 1613
QY 421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
DB 1614 GAGGAAGCAAAAGATATTGTCAGGCTCTCTTGGCTAAGAAACACAGACCAACGCTTAGGA 1673
QY 441 SerArgGluLysSerAspAspProArgLysHisPhePheLysThrIleAsnPhePro 460
DB 1674 AGCAGAGAAAGTCTGATGATCCCAAGAAACATCATCTTTTAAACGATCAACTTTTCT 1733
QY 461 ArgLeuGluAlaGlyLeuIleGluProPheValProAspProSerValValTyrAla 480
DB 1734 CGCTGGGAAGCTGGCTAATGAACCCCATTTGTCAGACCCCTTCAGTGGTTATGCC 1793
QY 481 LysAspIleAlaGluAlaAspPheSerGluValArgGlyValGluPheAspAspLys 500
DB 1794 AAAGACATCGCTGAAATTTGATGATTTCTCGAGGTTCGGGGGTGGAATTTGATGACAAA 1853
QY 501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTyrGlnGlu 520
DB 1854 GATAAGCAGTTCCTTCAAAACATTTTCGACAGCTGCTGTTCTATAGCATGCGCAGGAAGA 1913
QY 521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
DB 1914 ATTATAGAAACGGGACTGTTTGAGAACTGAATGATGACCCCAACAGACCTACGGTTGTGAG 1973
QY 541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
DB 1974 GAGGTAATTCATCCAAAGCTGGCGTGTGTTGTTATTG 2012

RESULT 9
US-10-217-745-5
; Sequence 5, Application US/10217745
; Publication No. US20030004328A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Milgowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. US20030004328A1el Human G-Coupled Protein Receptor Kinases an
; TITLE OF INVENTION: Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/10/217,745
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US/09/802,117
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2249
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-217-745-5

Alignment Scores:
Pred. No.: 0 Length: 2249
Score: 2883.00 Matches: 552
Percent Similarity: 99.82% Conservative: 0
Best Local Similarity: 99.82% Mismatches: 1
Query Match: 99.79% Indels: 0
DB: 14 Gaps: 0

US-10-044-205A-2 (1-553) x US-10-217-745-5 (1-2249)
QY 1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
DB 354 ATGTGGACATGGGGGCCCTGGACACACCTGATCGCCACACACCGCTACTCTGAGGCCCGG 413
QY 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgSerLeuAlaLeuPro 40
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DB 414 AAGCCCTCGGACTCGCAGCAAGAGCTGCAGCGCGCGCGCTAGCCTGGCCCTGCCCC 473
QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAenPheHisSerLeuCys 60
DB 474 GGGCTGAGGGCTCGCGGGAGCTCCGCGAGAGCTGCTCCCTGAACTTCCACAGCCTGTGT 533
QY 61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
DB 534 GAGCAGCAGCCCATCGCTCGCGGCTCTTCGTCGACTTCTTAGCCACAGTGCACCGTTC 593
QY 81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
DB 594 CGCAAGCGCGCAACTTCTTAGAGGAGCTGCAGAACTGGGAGCTGGCGAGGAGGAGGCC 653
QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
DB 654 ACCAAAGACACGCGCTGCAGGGCTGTGGCCACTTGTGCGAGTGGCCCTGCCCCGGG 713
QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
DB 714 AACCCGCAACCTTCTCAGCCAGCGCTGGCCACCAAGTGCACAGCAGCCACCACTGAG 773
QY 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
DB 774 GAAGAGCAGTGGCTGCAGTGACGCTGCCAAGCTGAGGCTATGGCTTTCTTGCACAGAG 833
QY 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
DB 834 CAGCCCTTTAAGGATTTCTGACAGCGCCCTTCTACGACCAAGTTCGTGAGTGGAAACTC 893
QY 181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
DB 894 TTCGAGATGCAACCCAGTGTGACACAGTACTTCTACTGAGTTCAGAGTCTGGGGNAGGT 953
QY 201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
DB 954 GGTTTTGGGGAGGTATGTGCGCTCAGGTGAAAAACACTGGGAAAGATGTATGCTCTGAAG 1013
QY 221 LysLeuAspLysValLysArgLeuLysLysGlyGlyGlyLysMetAlaLeuLeuLys 240
DB 1014 AACTGACACAGAGCGCTGGAAGAAAGGTGGGAGAAAGATGGCTCTCTTGGAAAG 1073
QY 241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
DB 1074 GARATCTTGGAGAGGTGACAGCCCTTCTCATCTCTCTGCGCTATGCTTTGAGAGC 1133
QY 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
DB 1134 AAGACCATCTCTGCTTGTGATGAGCTGATGAATGGGGGAGACCTCAAGTTCACATC 1193
QY 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
DB 1194 TACAACGTGGGACGCGCTGGACATGAGCGGGTGATCTTTTACTCTGGCCAGATA 1253
QY 301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
DB 1254 GCCTGTGGATGCTGCACCTCCATGAACTCGGCATGCTATCTCGGACATGAAGCCTGAG 1313
QY 321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
DB 1314 AATGTGCTTCTGGATGACCTCGGCAACTGCAAGGTATATGACCTGGGGCTGGCGGTGAG 1373
QY 341 MetLysGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
DB 1374 ATGAAGGTGGCAAGCCCATCACCAGAGGCTGGAAACCAATGTTACATGGCTCTCTGAG 1433
QY 361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
DB 1434 ATCTTAATGAAAGGTAAAGTTATCTCTCTGCTGAGCTGGTTTGGCATGGGATGACG 1493
QY 381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
DB 1494 ATTTATGAAATGGTGTGCTGGACGAACCACTTCAAGAGTTTACAAGGAAAGGTGAGTAAA 1553
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QY 401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAenPheThr 420
DB 1554 GAGGATCTGAGCAAGAACTCTGCAAGACGAGGTCAAAATTCAGCATGATTAATTCACA 1613
QY 421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
DB 1614 GAGGAAGCAAGATATTTGCGAGGCTCTTTGGCTAAGAAACCAAGAGCAACGCTTAGGA 1673
QY 441 SerArgGluLysSerAspAspProArgLysHisPhePheLysThrIleAenPhePro 460
DB 1674 AGCAGAGAAAGTCTGATGATCCAGGAAACATCATTTCTTTAAAGATCACTTTCTCT 1733
QY 461 ArgLeuGluAlaGlyLeuIleGluProPheValProAspProSerValValTyrAla 480
DB 1734 CGCTTGAAGCTGGCTTAATTAAGACCCCATTTGTGCCAGACCCCTTCACTGCTTTATGCC 1793
QY 481 LysAspIleAlaGluLysAspPheSerGluValArgGlyValGluPheAspPheLys 500
DB 1794 AAGACATCGCTGAATGATATTTCTGAGGTTTCGGGGGTGGAATTTGATGACAAA 1853
QY 501 AspLysGlnPhePheLysAenPheAlaThrGlyAlaValProIleAlaIleAlaIleGlu 520
DB 1854 GATAGCAGTCTTCAAAACTTTCGACAGGTGCTGTTCTTATAGCATGGCAGGAGNA 1913
QY 521 IleIleGluThrGlyLeuPheGluGluLeuAenAspProAenArgProThrGlyCysGlu 540
DB 1914 ATTATAGAAACGGGACTGTTTCAGGAACCTGAATGACCCCAACAGACCTACGGGTTGTGAG 1973
QY 541 GluGlyAenSerSerLysSerGlyValCysLeuLeuLeu 553
DB 1974 GAGGTAATTCATCAAGTCTGGCGTGTGTTGTTATTG 2012

RESULT 10

US-09-964-469-1
; Sequence 1, Application US/09964469
; Patent No. US20020034803A1
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEROSF
; FILE REFERENCE: CL000636DIV
; CURRENT APPLICATION NUMBER: US/09/964,469
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 60/208,331
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: 09/738,894
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Human
US-09-964-469-1

Alignment Scores:
Pred. No.: 0 Length: 1662
Score: 2876.00 Matches: 551
Percent Similarity: 99.64% Conservative: 0
Best Local Similarity: 99.64% Mismatches: 2
Query Match: 99.55% Indels: 0
DB: 9 Gaps: 0

US-10-044-205A-2 (1-553) x US-09-964-469-1 (1-1662)

QY 1 MetValAspMetGlyValLeuAspAenLeuIleAlaAenThrAlaTyrLeuGlnAlaArg 20
DB 1 ATGGTGGACATGGGGCCCTGGACAACTGATCGCCCAACACCGCTACTCTGAGGCCCGG 60
QY 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgSerLeuAlaLeuPro 40

DB 61 AAGCCCTCGGACTGGCAGCAGCAAGAGCTGCAGCGCGCGCGGTAGCTGGCCCTGCCCC 120
QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAenPheHisSerLeuCys 60
DB 121 GGGCTGCAAGGCTGCGCGAGCTCGCCAGAAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
QY 61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
DB 181 GAGCAGCAGCCCATCGGTGCGCGCTTCCGTGTGACTTCTTACGCCACAGTGGCCACGTTT 240
QY 81 ArgLysAlaAlaThrPheLeuGluAspValGlnAenTTPGluLeuAlaGluGlyPro 100
DB 241 GCGAAGCGCGCAACCTTCTAGAGACCTGCAAACTGGGAGCTGGCCGAGGAGGACCC 300
QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
DB 301 ACCAAAGACAGCGGCTGCGAGGGCTGTGGCCACTTGTGGAGTGGCCCTGCCCGGGG 360
QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
DB 361 AACCGCAACCTTCTCAGCCAGCGCTGGCCACCAAGTGCACAGCAGCCACCACTGAG 420
QY 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
DB 421 GAAGAGCAGGTGGCTGCGAGTGCAGCTGGCCAGGCTGAGGCCCATGGCTTCTTTCGAAG 480
QY 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
DB 481 CAGCCCTTTAAGGATTTCTGACAGCGCTTCTACGACAAAGTTTCTGCAGTGGAACTC 540
QY 181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
DB 541 TTCAGATGCAACCAAGTGTGACAAAGTACTTCTACTGAGTTTCAGAGTGTGGGGAAGGT 600
QY 201 GlyPheGlyGluValCysAlaValGlnValLysAenThrGlyLysMetTyrAlaCysLys 220
DB 601 GGTITTTGGGAGGTATGTGCCCTCAGGTGAAACACTGGGAAGATGTATGCCCTGTAAG 660
QY 221 LysLeuAspLysLysArgLeuLysLysGlyGlyGlyLysMetAlaLeuLeuGluLys 240
DB 661 AAATCGACAGAGGCGCTGAGAGAAAGGTGGCGAGAGATGCTCTCTTGGAAAG 720
QY 241 GluLeuLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
DB 721 GAAATCTTGGAGAAGGTGAGCAGCCCTTCTATTTGTCTCTGGCTATGCTCTTGGAGC 780
QY 261 LysThrHisLeuCysLeuValMetSerLeuMetAenGlyGlyAspLysPheHisIle 280
DB 781 AAGACCCCATCTCTGCCCTTGTATGAGCTGATGAATGGGGAGAGCTCAAGTTCCACATC 840
QY 281 TyrAenValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
DB 841 TACAACTGGGCAAGCGCTGGCTGACATGAGCGGGTGATCTTTTACTCGGCCAGATA 900
QY 301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
DB 901 GCCTGTGGATGCTGCACCTCATGAACTCGCATCGTCTATCGGACATGAAGCTGAG 960
QY 321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
DB 961 AATGTGCTTCTGGATGACCTCGCAACCTGCAAGTTATCTGACCTGGGGCTGGCCGTGAG 1020
QY 341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAenGlyTyrMetAlaProGlu 360
DB 1021 ATGAAGGTGGCAAGCCCATCCACAGAGGCTGGAACCAATGGTTATACCTGCTCTGAG 1080
QY 361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
DB 1081 ATCTAATGGGAAGGTAAAGTTATTTCTTATCTCTGTGGACTGTTTGGCCATGGGATGAGC 1140
QY 381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
DB 1141 ATTTATGAATGGTGTGGAGCAACCACTTCAAGAGATTACAAAGAAAGGTTCAGTAAA 1200

QY 401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
 DB 1201 GAGGATCTGAGCAAGAACTCTGCAAGACAGAGTCAAAATTCAGCATGATTAACCTTCA 1260
 QY 421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
 DB 1261 GAGGAAGCAAAAGATATTTCAGGCTCTTCTGGCTTAAGAAACAGAGCAACGCTTAGGA 1320
 QY 441 SerArgGluLysSerAspAspProArgLysHisHisPhePheLysThrIleAsnPhePro 460
 DB 1321 AGCAGAGAAAGTCTGATGATCCAGGAAACATCATTTCTTTAAACCGATCAACTTCTCT 1380
 QY 461 ArgLeuGluAlaGlyLeuIleGluProPhePheValProAspProSerValValTyrAla 480
 DB 1381 CGCTGGAGCTGGCTTAATGACCCCAATTTGTGCCAGACCTTCAGTGGTTTATGCC 1440
 QY 481 LysAspIleAlaGluLeuAspPheSerGluValArgGlyValGluPheAspAspLys 500
 DB 1441 AAAGACATCGCTGAATTCATGATTTCTGAGGTTCCGGGGTGGAAATTTGATGACAAA 1500
 QY 501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTTPGlnGluGlu 520
 DB 1501 GATAAGCAGTTCTTCAAAACATTTGCGACAGGTGCTGTTCTTATAGCATGGCAGGAAGA 1560
 QY 521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
 DB 1561 ATTATAGAAACGGAGCTGTTTCAGGACTGATGATGACCCCAACAGACCTACGGTTGTG 1620
 QY 541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
 DB 1621 GAGGGTAATTCATCCAAAGTCTGCGGTGTTGTTGTTATTG 1659

RESULT 11

US-10-425-962-1

; Sequence 1, Application US/10425962
 ; Publication NO. US20030180786A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GUEGLER, Karl et al
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
 ; ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 ; TITLE OF INVENTION: THERSOF
 ; FILE REFERENCE: CL000636DIV2
 ; CURRENT APPLICATION NUMBER: US/10/425,962
 ; PRIOR FILING DATE: 2003-04-30
 ; PRIOR APPLICATION NUMBER: 09/964,469
 ; PRIOR FILING DATE: 2001-09-28
 ; PRIOR APPLICATION NUMBER: 09/738,894
 ; PRIOR FILING DATE: 2000-12-18
 ; PRIOR APPLICATION NUMBER: 60/208,331
 ; PRIOR FILING DATE: 2000-06-01
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 1662
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-425-962-1

Alignment Scores:

Pred. No.: 0 Length: 1662
 Score: 2876.00 Matches: 551
 Percent Similarity: 99.64% Conservative: 0
 Best Local Similarity: 99.64% Mismatches: 2
 Query Match: 99.55% Indels: 0
 DB: 16 Gaps: 0

US-10-044-205A-2 (1-553) x US-10-425-962-1 (1-1662)

QY 1 MetValAspMetGlyAlaIleAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
 DB 1 ATGTGGGACATGGGGGCGCTGGACAACTGATGCGCAACACCGGCTACTCGAGCGCGG 60

QY 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgSerLeuAlaLeuPro 40
 DB 61 AAGCCCTCGGACTGGCAGCAGCAAGAGCTGCAGCGGCGCGGCTAGCTGGCCCTGGCCC 120
 QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
 DB 121 GGGCTGCAGGGCTGCGCGAGCTCCGCAGAAAGCTGTCCCTGAACTTCCACAGCCCTGTGT 180
 QY 61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
 DB 181 GAGCAGCAGCCCATCGGTGCGCGCTCTTCGTGACTTCTTAGCCACAGTCCCAACGTTTC 240
 QY 81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTTPGluLeuAlaGluGluGlyPro 100
 DB 241 CGCAAGCGGGCAACCTTCTTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300
 QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
 DB 301 ACCAAGACAGCGCGCTGCAGGGCTGTGTGCCACTTGTGCGAGTGTCCCTGCCCGGGG 360
 QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
 DB 361 AACCCGCAACCTTCTTCAGCCAGCGGTGCCCAAGTCCCAAGCAGCAGCCACTGAG 420
 QY 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
 DB 421 GAAGCGCAGTGGCTGCAGTGCAGCTGCCCAAGGCTGAGGCCATGGCTTCTTTCGAAGAG 480
 QY 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTTPLysLeu 180
 DB 481 CAGCCCTTTAAGGATTTCTGACCAAGCGCTTCTACGACAAGTTCTTCAGTGGAAATC 540
 QY 181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
 DB 541 TTCGAGATGCAACCAAGTGTGACAGTACTTCTACTGAGTTCAGAGTCTCGGGGAAAGGT 600
 QY 201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
 DB 601 GGTTTTGGGAGGTATGTGCGCTCCAGGTGAAACACTGGGAAGATGTATGCTGTGAAG 660
 QY 221 LysLeuAspLysLysArgLeuLysLysGlyGlyGlyLysMetAlaLeuLeuGluLys 240
 DB 661 AAACCTGGACAAGAGCGCTGCAAGAAAGGTGGCGAAGATGGGTCTCTTGGMAAAG 720
 QY 241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
 DB 721 GAAATCTTTGGAAAGGTGACAGCCCTTTCATGCTCTCTGCGCTATGCTTTTGAGAGC 780
 QY 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
 DB 781 AAGACCCATCTCTGCTTGTGATGAGCTGATGATGAGTGGGGGAGACCTCAAGTTCACATC 840
 QY 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
 DB 841 TACAACGTGGGCACGCGTGGCTGACATGAGCGGGTGTATCTTTTACTCTGCGCCAGATA 900
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 QY 361 IleLeuMetGluLysValSerTyrSerTyrProValAspTTPPheAlaMetGlyCysSer 380
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Db 1201 GAGGATCTGAGCAAGCAAGAACTCTGCAAGCAGAGGTCAATTCAGCATGATAACTTCACA 1260
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Db 1321 AGCAGAGAAAGTCTGATGATCCCAAGGAAACATCATTTCTTAAACCATCAACTTCTCT 1380
Qy 461 ArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValValPheAla 480
Db 1381 CGCTGTGAAGCTGGCTAATTGAACCCCACTTTGTGCCAGACCCCTTCAGTGGTTATGCC 1440
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Db 1501 GATAAGCAGTTCCTTCAAAACACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGA 1560
Qy 521 IleIleGluThrGlyLeuPheGluLeuLeuAsnAspProAsnArgProThrGlyCysGlu 540
Db 1561 ATTATAGAAACGGGACTGTTTGGAGAACTGAATGACCCCAACAGACCTACCGGTTGTGAG 1620
Qy 541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
Db 1621 GAGGTAATTCATCCAGTCTGGCGTGTGTTGTTATTG 1659
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; Sequence 273, Application US/10072012
; Publication No. US20040033493A1
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; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zethusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier, Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsbrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31

; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 273
; LENGTH: 1701
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-072-012-273

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Score: 2823.50 Matches: 547
Percent Similarity: 98.56% Conservative: 0
Best Local Similarity: 98.56% Mismatches: 1
Query Match: 97.73% Indels: 7
DB: 17 Gaps: 3

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Qy 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgSerLeuAlaLeuPro 40
Db 79 AAGCCCTCGGACTCGACAGCAAGAGCTGCGAGGGCGGCGGTAGCTTGCCCTGCCCC 138
Qy 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysSerLeuAsnPheHisSerLeuCys 60
Db 139 GGGCTGACGGCTGCGGGAGCTCGCCAGAAAGCTGCTCCCTGAACTTCCACAGCTGTGT 198
Qy 61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
Db 199 GAGCAGCAGCCCATCGGTGCGGCTCTTCCGTGACTTCTTAGCCACAGTGCACAGTTC 258
Qy 81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGlyPro 100
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Qy 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
Db 379 AACCCGCNACCTTCTTCAGCAGCCGCTGGCCACCAAGTGCACAGCAGCCACTGAG 438
Qy 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
Db 439 GAAGAGCGAGTGGCTGCGAGTCAGTCGCTGGCAAGGCTGAGGCCATGGCTTCTTGAAGAG 498
Qy 161 GlnProPheLysAspPheValThrSerAlaPheTyAspLysPheLeuGlnTrpLysLeu 180
Db 499 CAGCCCTTAAAGGATTTCTGACAGCCGCTTCTACGACAAAGTTCCTCGAGTGGAAATC 558
Qy 181 PheGluMetGlnProValSerAspLysTyThrPheThrGluPheArgValLeuGlyLysGly 200
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/ CURRENT APPLICATION NUMBER: US/09/964,469
/ CURRENT FILING DATE: 2001-09-28
/ PRIOR APPLICATION NUMBER: 60/208,331
/ PRIOR FILING DATE: 2000-06-01
/ PRIOR APPLICATION NUMBER: 09/738,894
/ PRIOR FILING DATE: 2000-12-18
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 3
/ LENGTH: 36651
/ TYPE: DNA
/ ORGANISM: Human
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (1)...(36651)
/ OTHER INFORMATION: n = A,T,C or G
US-09-964-469-3

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Pred. No.: 2,23e-165 Length: 36651
Score: 1528.00 Matches: 349
Percent Similarity: 41.40% Conservative: 0
Best Local Similarity: 41.40% Mismatches: 1
Query Match: 52.89% Indels: 493
DB: 9 Gaps: 1

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Db |
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Db |
QY 2196 GGGCTGCGAGGGTGGCGGAGCTCCGCCAGAGCTGTCCCTGAACTTCACAGCCTGTGT 2255
QY 61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
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QY 2256 GAGCAGCAGCCCATCGCTCGCGCCCTTCCGTGACTTCTTAGCCACAGTGCACAGTTC 2315
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QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY NUC
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Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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22	373	17.0	2529	4	US-09-417-197-42
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28	311.6	14.2	1886	1	US-07-980-526-1	Sequence 1, Appli
29	311.6	14.2	1975	4	US-09-614-748A-9	Sequence 9, Appli
30	253.2	11.5	1305	4	US-09-614-748A-12	Sequence 12, Appli
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32	151	6.9	3422	4	US-09-949-016-1312	Sequence 1312, Ap
33	130.8	6.0	2067	4	US-09-016-434-1306	Sequence 1306, Ap
34	129.2	5.9	3628	4	US-09-949-016-4773	Sequence 4773, Ap
35	127.6	5.8	2362	4	US-09-620-312D-273	Sequence 273, App
36	116.4	5.3	294	1	US-08-221-817-9	Sequence 9, Appli
37	116.4	5.3	294	1	US-08-454-439-9	Sequence 9, Appli
38	116.4	5.3	294	5	PCT-US94-10487-9	Sequence 9, Appli
39	112.8	5.1	2599	6	5266484-1	Patent No. 5266464
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41	112	5.1	1788	4	US-09-417-197-68	Sequence 68, Appli
42	110.8	5.0	1191	4	US-09-841-683-10	Sequence 10, Appli
43	110.8	5.0	1224	4	US-09-841-683-8	Sequence 8, Appli
44	110.8	5.0	1485	4	US-09-801-876B-1	Sequence 1, Appli
45	110.8	5.0	1485	4	US-10-254-869-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-802-117-5
; Sequence 5, Application US/09802117
; Patent No. 644456
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilgowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 644456el Human G-Coupled Protein Receptor Kinases and Polyn
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/09/802,117
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/189,449
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2249
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-802-117-5

Query Match	91.4%	Score 2008.8;	DB 3;	Length 2249;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 2010;	Conservative	0;	Mismatches	2;
Indels	0;	Gaps	0;	
Qy	175	CAGGCCACAGGACTCAGCTGTAATCCCTTGGAGCTGTCTCACCCGGGAGGGAAGCAG	234	
Db	238	CAGGCCACAGGACTCAGCTGTAATCCCTTGGAGCTGTCTCACCCGGGAGGGAAGCAG	297	
Qy	235	CCAGCAGCCCTCCAGCCCTCTTGTGCTTTCCTTGGAGTGCGCCCGCTGCTCAGCCATGG	294	
Db	298	CCAGCAGCCCTCCAGCCCTCTTGTGCTTTCCTTGGAGTGCGCCCGCTGCTCAGCCATGG	357	
Qy	295	TGGACATGGGGCCCTTGACACCTGTATCGCCMACACCGCTTACCTGCAGGCCCGGAGC	354	
Db	358	TGGACATGGGGCCCTTGACACCTGTATCGCCMACACCGCTTACCTGCAGGCCCGGAGC	417	
Qy	355	CCTCGGACTCGCACAGCAAGAGCTGCGAGCGCGCGGTAGCTGGCCCTCGCCCGGC	414	
Db	418	CCTCGGACTCGCACAGCAAGAGCTGCGAGCGCGCGGTAGCTGGCCCTCGCCCGGC	477	
Qy	415	TGCAGGGCTGCGCGAGCTCCGCCAAGAGCTGTTCCTGAACCTTCACAGCCCTGTGTGAGC	474	
Db	478	TGCAGGGCTGCGCGAGCTCCGCCAAGAGCTGTTCCTGAACCTTCACAGCCCTGTGTGAGC	537	
Qy	475	AGCAGCCCATCGGTGCGCCCTCTTCCGTGACTTCTTAGCCACAGTCCACAGCTTCCGCA	534	
Db	538	AGCAGCCCATCGGTGCGCCCTCTTCCGTGACTTCTTAGCCACAGTCCACAGCTTCCGCA	597	


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; PRIOR APPLICATION NUMBER: US 60/188,449
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: homo sapiens
; US-09-802-117-1

Query Match      75.5%; Score 1658.4; DB 3; Length 1662;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1659; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 291 ATGTGGAGATGGGGGCTGGACAACTGATCGCAACACGCGCTACTCGAGGCGCGG 350
Db 1 ATGTGGAGATGGGGGCTGGAAACCTGATCGCAACACGCGCTACTCGAGGCGCGG 60
QY 351 AAGCCCTCGGACTGGACAGCAAGAGCTGAGCGCGCGCGGTAGCTGGCCCTGGCC 410
Db 61 AAGCCCTCGGACTGGACAGCAAGAGCTGAGCGCGCGCGGTAGCTGGCCCTGGCC 120
QY 411 GGGCTGCAAGGCTGGCGGAGCTCGCGCAGAGCTGTCCCTGAACTTCCACAGCCTGTGT 470
Db 121 GGGCTGCAAGGCTGGCGGAGCTCGCGCAGAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
QY 471 GAGCAGCAGCCCATCGGTGCGCGCTCTTCGTGACTTCTAGCCACAGTGCACAGTTC 530
Db 181 GAGCAGCAGCCCATCGGTGCGCGCTCTTCGTGACTTCTAGCCACAGTGCACAGTTC 240
QY 531 CSCAAGGCGCAACTTCTAGAGAGCTGAGAGAGCTGGAGCTGGCGAGGAGGAGCC 590
Db 241 CSCAAGGCGCAACTTCTAGAGAGCTGAGAGAGCTGGAGCTGGCGAGGAGGAGCC 300
QY 591 ACCAAGAAGCAGCGGCTGAGGCGGCTGGTGGCACTTGTGCAAGTGGCCCTGGCCGGG 650
Db 301 ACCAAGAAGCAGCGGCTGAGGCGGCTGGTGGCACTTGTGCAAGTGGCCCTGGCCGGG 360
QY 651 AACCCGCAACCTTCTGACAGGCGCTGGCCACCAAGTGCAGAGCCACCACTGAG 710
Db 361 AACCCGCAACCTTCTGACAGGCGCTGGCCACCAAGTGCAGAGCCACCACTGAG 420
QY 711 GAAGAGCAGTGGCTGCACTGAGCGTGCAGAGGCTGAGGCGCATGGCTTCTTGAAGAG 770
Db 421 GAAGAGCAGTGGCTGCACTGAGCGTGCAGAGGCTGAGGCGCATGGCTTCTTGAAGAG 480
QY 771 CAGCCCTTTAAGATTTGAGTCCAGCGCTTCTAGCAAGATTTCTGCAAGTGGAACTC 830
Db 481 CAGCCCTTTAAGATTTGAGTCCAGCGCTTCTAGCAAGATTTCTGCAAGTGGAACTC 540
QY 831 TTGAGATGCAACCGAGTGCAGAGTACTTCACTGAGTGCAGAGTGTGGGGAAGGT 890
Db 541 TTGAGATGCAACCGAGTGCAGAGTACTTCACTGAGTGCAGAGTGTGGGGAAGGT 600
QY 891 GGTTTTGGGAGATGTGCGCGTCCAGAGTGAAAAACACTGGGAAGATGTATCGCTGAAG 950
Db 601 GGTTTTGGGAGATGTGCGCGTCCAGAGTGAAAAACACTGGGAAGATGTATCGCTGAAG 660
QY 951 AAACCTGGAACAAGCGGCTGAAGAAAGAGTGGCGAAGATGGCTCTCTTGGAAAG 1010
Db 661 AAACCTGGAACAAGCGGCTGAAGAAAGAGTGGCGAAGATGGCTCTCTTGGAAAG 720
QY 1011 GAAATCTTGGAGAGTGCAGAGCCCTTTCATTGTCTCTGCGCTATGCTTGGAGAGC 1070
Db 721 GAAATCTTGGAGAGTGCAGAGCCCTTTCATTGTCTCTGCGCTATGCTTGGAGAGC 780
QY 1071 AAGACCCATCTCTGCGCTTGTGATGAGCCTGATGAATGGGGAGACCTCAAGTTCCACATC 1130
Db 781 AAGACCCATCTCTGCGCTTGTGATGAGCCTGATGAATGGGGAGACCTCAAGTTCCACATC 840
QY 1131 TACAAGCTGGGACGCGTGGCTGGACATGAGCGCGGTGATCTTTTACTCGGCCAGATA 1190
Db 841 TACAAGCTGGGACGCGTGGCTGGACATGAGCGCGGTGATCTTTTACTCGGCCAGATA 900
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QY 1191 GCCTGTGGGATGCTGCACCTCCATGAACCTCGCATCGTCTATCGGACATGAAGCCTGAG 1250
Db 901 GCCTGTGGGATGCTGCACCTCCATGAACCTCGCATCGTCTATCGGACATGAAGCCTGAG 960
QY 1251 AATGTGCTTCTGGATGACCTCGGCAACTGCAAGTATCTGACCTGGGGCTGGCGTGGAG 1310
Db 961 AATGTGCTTCTGGATGACCTCGGCAACTGCAAGTATCTGACCTGGGGCTGGCGTGGAG 1020
QY 1311 ATGAGGGTGGCAAGCCCATCAACCCAGAGGCTGGACCAATGTTATCATGGCTCCCTGAG 1370
Db 1021 ATGAGGGTGGCAAGCCCATCAACCCAGAGGCTGGACCAATGTTATCATGGCTCCCTGAG 1080
QY 1371 ATCTTAATGAAAAAGGTAAAGTTATTTCTATCTCTGAGCTGGTTTGGCATGGGATGCAGC 1430
Db 1081 ATCTTAATGAAAAAGGTAAAGTTATTTCTATCTCTGAGCTGGTTTGGCATGGGATGCAGC 1140
QY 1431 ATTTATGAAATGTTGCTGGAAGCAACCAATTAAGATTAAGAGAAAGGTGAGTAA 1490
Db 1141 ATTTATGAAATGTTGCTGGAAGCAACCAATTAAGATTAAGAGAAAGGTGAGTAA 1200
QY 1491 GAGGATCTGAGCAAGCAACTCTGCAAGAGAGGTCAAATTCAGCATGATACTTACA 1550
Db 1201 GAGGATCTGAGCAAGCAACTCTGCAAGAGAGGTCAAATTCAGCATGATACTTACA 1260
QY 1551 GAGGATCTGAGCAAGCAACTCTGCAAGAGAGGTCAAATTCAGCATGATACTTACA 1610
Db 1261 GAGGATCTGAGCAAGCAACTCTGCAAGAGAGGTCAAATTCAGCATGATACTTACA 1320
QY 1611 AGCAGAGAAAGTCTGATGATCCAGGAAACATCAATTTCTTAAACGATCAACTTTTCT 1670
Db 1321 AGCAGAGAAAGTCTGATGATCCAGGAAACATCAATTTCTTAAACGATCAACTTTTCT 1380
QY 1671 CGCTTGAAGCTGGCCCTAAATTTGAACCCCACTTCTGCGCAGACCCCTTCACTGGTTATGCC 1730
Db 1381 CGCTTGAAGCTGGCCCTAAATTTGAACCCCACTTCTGCGCAGACCCCTTCACTGGTTATGCC 1440
QY 1731 AAAGACATCGCTGAAATTTGATGATTTCTCTGAGGTTGGGGGGTGGAAATTTGATGACAAA 1790
Db 1441 AAAGACATCGCTGAAATTTGATGATTTCTCTGAGGTTGGGGGGTGGAAATTTGATGACAAA 1500
QY 1791 GATAGAGCTTTCTCAAAACTTTTGGACAGTCTGTTCTCTATAGCATGCGAGGAGAA 1850
Db 1501 GATAGAGCTTTCTCAAAACTTTTGGACAGTCTGTTCTCTATAGCATGCGAGGAGAA 1560
QY 1851 ATTATAGAAACGGGACTGTTTGAAGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1910
Db 1561 ATTATAGAAACGGGACTGTTTGAAGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
QY 1911 GAGGTAATTCATCAAGCTGGCGTGGTGTGTTTATTTGTA 1952
Db 1621 GAGGTAATTCATCAAGCTGGCGTGGTGTGTTTATTTGTA 1662
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RESULT 4
US-10-217-745-1
; Sequence 1, Application US/10217745
; Patent No. 6838275
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilgowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6838275el Human G-Coupled Protein Receptor Kinases and
; TITLE OF INVENTION: Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/10/217,745
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US/09/802,117
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
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Qy	291	ATGTTGACATGCGGGCCCTGGACAACCTGATCCCAACACCGCCTACTCTGAGGCCCGG	350
Db	1	ATGTTGACATGCGGGCCCTGGACAACCTGATCGCCAACACCGCTACTCTGACGCCCGG	60
Qy	351	AAGCCCTCGACATCGCACACAAAGAGCTGCAGCGCGCGCGTGAACCTGGCCCTGSCC	410
Db	61	AAGCCCTCGACATCGCACACAAAGAGCTGCAGCGCGCGCGTGAACCTGGCCCTGSCC	120
Qy	411	GGGCTGAGGGCTGCGCGGAGCTCCGCAGAAAGCTGTCCTGAACTTCCACAGCCTGTGT	470
Db	121	GGGCTGAGGGCTGCGCGGAGCTCCGCAGAAAGCTGTCCTGAACTTCCACAGCCTGTGT	180
Qy	471	GAGCAGAGCCCATCGTGTGCGCGCTCTTCGTGATCTTCTAGCCACAGTGCACCGTTC	530
Db	181	GAGCAGAGCCCATCGTGTGCGCGCTCTTCGTGATCTTCTAGCCACAGTGCACCGTTC	240
Qy	531	CGAAGCGGCAACCTTCTTAGAGGAGCTGCAGAACTGGGAGCTGGCCGAGGAGGACCC	590
Db	241	CGAAGCGGCAACCTTCTTAGAGGAGCTGCAGAACTGGGAGCTGGCCGAGGAGGACCC	300
Qy	591	ACCAAGAAGCAGCGCGCTGCGAGGGGCTGGTGGCCACTTGTGCGAGTGCCCTGCCCGGGG	650
Db	301	ACCAAGAAGCAGCGCGCTGCGAGGGGCTGGTGGCCACTTGTGCGAGTGCCCTGCCCGGGG	360
Qy	651	AACCCGCAACCTTCTCAGCCAGCGCGTGCCACCAAGTGCCAAAGCAGCAACACTGAG	710
Db	361	AACCCGCAACCTTCTCAGCCAGCGCGTGCCACCAAGTGCCAAAGCAGCAACACTGAG	420
Qy	711	GAAGAGCGAGTGCGTCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAGAG	770
Db	421	GAAGAGCGAGTGCGTCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAGAG	480
Qy	771	CAGCCCTTTAAGGATTTTCGTGACCAGCGCCCTCTTACGACAAGTTTCTGCAGTGAAACTC	830
Db	481	CAGCCCTTTAAGGATTTTCGTGACCAGCGCCCTCTTACGACAAGTTTCTGCAGTGAAACTC	540
Qy	831	TTGAGATGCAACCAAGTGTGAGCAAGTATCTCACTGAGTTCAGAGTCTGGGGAAAGGT	890
Db	541	TTGAGATGCAACCAAGTGTGAGCAAGTATCTCACTGAGTTCAGAGTCTGGGGAAAGGT	600
Qy	891	GGTTTTGGGAGGTATCTGCGCTCCAGGTGAAAACACTGGGAGAGTATGCTGTGAAG	950
Db	601	GGTTTTGGGAGGTATCTGCGCTCCAGGTGAAAACACTGGGAGAGTATGCTGTGAAG	660
Qy	951	AAACTGCACAAGACCGGCTGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG	1010
Db	661	AAACTGCACAAGACCGGCTGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG	720
Qy	1011	GAATCTTGGAAAGGTGACAGCCCTTTCAATTGCTCTCTGGCCATAGCTTTGAGAGC	1070
Db	721	GAATCTTGGAAAGGTGACAGCCCTTTCAATTGCTCTCTGGCCATAGCTTTGAGAGC	780
Qy	1071	AAGACCCATCTCTGCTTGTATGAGCCTGATGAATGGGGAGACCTCAAGTTCACATC	1130
Db	781	AAGACCCATCTCTGCTTGTATGAGCCTGATGAATGGGGAGACCTCAAGTTCACATC	840
Qy	1131	TACAACTGGGACGCGTGGCTGGACAATGAGCCGGGTGATCTTTTACTCGGCCACATA	1190
Db	841	TACAACTGGGACGCGTGGCTGGACAATGAGCCGGGTGATCTTTTACTCGGCCACATA	900
Qy	1191	GCCTGTGGGATGTGCACCTCCATGAACCTCGGCATCGTCTATCGGACATCAAGCCCTGAG	1250
Db	901	GCCTGTGGGATGTGCACCTCCATGAACCTCGGCATCGTCTATCGGACATCAAGCCCTGAG	960
Qy	1251	AATGTGCTTCTGGATGACCTCGGCAACTGCAAGGTTATCTGACCTGGGGCTGGCCGTGGAG	1310
Db	961	AATGTGCTTCTGGATGACCTCGGCAACTGCAAGGTTATCTGACCTGGGGCTGGCCGTGGAG	1020
Qy	1311	ATGAAGGCTGCAAGCCCATCACCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG	1370
Db	1021	ATGAAGGCTGCAAGCCCATCACCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG	1080
Qy	1371	ATCCTAATGGAAGGTAAGTTATTCTCTATCTCTGGACCTGGTTTGGCATGGGATGCAGC	1430

[illegible]

RESULT 6

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RESULT 6
US-09-964-469-1
; Sequence 1, Application US/09964469
; Patent No. 6579709
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEROF
; FILE REFERENCE: CLO00636DIV
; CURRENT APPLICATION NUMBER: US/09/964,469
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 60/208,331
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: 09/738,894
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Human
US-09-964-469-1

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	Query Match	75.4%;	Score 1557.2;	DB 4;	Length 1662;
	Best Local Similarity	99.8%;	Pred. No. 0;		
	Matches 1659;	Conservative	Mismatches 0;	Indels 3;	Gaps 0;
Qy	291	ATGGTGGACATGGGGCCCTGACAAACCTGATCGGCAACACCGCCCTACTGACAGCCCGG	350		
Db	1	ATGGTGGACATGGGGCCCTGACAAACCTGATCGGCAACACCGCCCTACTGACAGCCCGG	60		
Qy	351	AAAGCCCTCGGACTGCGACACGAAAGAGCTGACAGCGCGCGCGCTAGCCTGCGCTTGCCC	410		

[illegible]

Db	1141	ATTTATGAAATGGTGTCTGGACGAACACCAATTCAAAGATTCAAGGAAAAGGTCAGTAAA	1200
Qy	1491	GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCACAGCATGATAACTTCACA	1550
Db	1201	GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCACAGCATGATAACTTCACA	1260
Qy	1551	GAGGAGCAAAGATATTTGCGAGCTCTTCTTGCTAAGAAAACAGAGCAACCGTTAGGA	1610
Db	1261	GAGGAGCAAAGATATTTGCGAGCTCTTCTTGCTAAGAAAACAGAGCAACCGTTAGGA	1320
Qy	1611	AGCAGAGAAAAGTCTGATGATCCCGAGAAACATCATTTCTTTAAAAACGATCAACTTTCCT	1670
Db	1321	AGCAGAGAAAAGTCTGATGATCCCGAGAAACATCATTTCTTTAAAAACGATCAACTTTCCT	1380
Qy	1671	CGCTGGAGAGTGGCCCTAAATGAAACCCCAATTTGTGCAGACGCTTCAGTGGTTTATGCC	1730
Db	1381	CGCTGGAGAGTGGCCCTAAATGAAACCCCAATTTGTGCAGACGCTTCAGTGGTTTATGCC	1440
Qy	1731	AAAGACATCGCTGAAATTTGATGATTTCTCTGAGGTTTCGGGGGTGGAAATTTGATGACAAA	1790
Db	1441	AAAGACATCGCTGAAATTTGATGATTTCTCTGAGGTTTCGGGGGTGGAAATTTGATGACAAA	1500
Qy	1791	GATTAAGCAGATTCTTCAAAAACCTTTGGCAGCAGGTGCTGTTCTTAGCATGGCAGGAAGAA	1850
Db	1501	GATTAAGCAGATTCTTCAAAAACCTTTGGCAGCAGGTGCTGTTCTTAGCATGGCAGGAAGAA	1560
Qy	1851	ATTATAGAAAACGGGACTGTTTGGAGAACTCAATGACCCCAACAGACTCAGGGTTGTGAG	1910
Db	1561	ATTATAGAAAACGGGACTGTTTGGAGAACTCAATGACCCCAACAGACTCAGGGTTGTGAG	1620
Qy	1911	GAGGGTAATTCATCCAAAGTCTGGCGTGTGTTTGTATTGTGAA	1952
Db	1621	GAGGGTAATTCATCCAAAGTCTGGCGTGTGTTTGTATTGTGAA	1662

RESULT 7

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US-09-802-117-3
; Sequence 3, Application US/09802117
; Patent No. 644456
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 64445661 Human G
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/09/802,117
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/188,449
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-802-117-3

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Query Match	47.6%	Score 1046.8;	DB 3;	Length 1052;
Best Local Similarity	99.8%	Pred. No. 3.4e-258;		
Matches 1048; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

Qy	291	ATGTTGACATGGGGCCCTGGACAACTGATGCCAACCCGCCTACTGTCAGGCCCGG	350
Db	1	ATGTTGACATGGGGCCCTGGACAACTGATGCCAACCCGCCTACTGTCAGGCCCGG	60
Qy	351	AAGCCCTCGACTCGGACAGCAAAAGACTGCAGCGCGCGGCGCTAGCTGGGCCCTGGCC	410
Db	61	AAGCCCTCGACTCGGACAGCAAAAGACTGCAGCGCGCGGCGCTAGCTGGGCCCTGGCC	120
Qy	411	GGGCTGAGGGCTCGCGGAGCTCCGCCAGAGCTGTCTCCCTGAACTTCCACAGGCTGTGT	470
Db	121	GGGCTGAGGGCTCGCGGAGCTCCGCCAGAGCTGTCTCCCTGAACTTCCACAGGCTGTGT	180


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QY 471 GAGCAGAGCCATCGCTCGCGCTCTTCGTGACTTCTTAGCCACAGTGCACAGCTTC 530
Db 181 GAGCAGAGCCATCGCTCGCGCTCTTCGTGACTTCTTAGCCACAGTGCACAGCTTC 240
QY 531 CGCAGGCGGCAACCTTCTTAGAGGACGTGAGAACTCGGAGCTGGCCGAGGAGGCC 590
Db 241 CGCAGGCGGCAACCTTCTTAGAGGACGTGAGAACTCGGAGCTGGCCGAGGAGGCC 300
QY 591 ACCAAGAAGCAGGCGCTCGAGGCGTGTGGCCACTTGTGGAGTGCCTTCCCGGGG 650
Db 301 ACCAAGAAGCAGGCGCTCGAGGCGTGTGGCCACTTGTGGAGTGCCTTCCCGGGG 360
QY 651 AACCCGCAACCTTCTTAGCAGCAGCGCTTCTAGCAAGTGCAGAGCAGCAACTGAG 710
Db 361 AACCCGCAACCTTCTTAGCAGCAGCGCTTCTAGCAAGTGCAGAGCAGCAACTGAG 420
QY 711 GAAGAGCGAGTGGCTGCAAGTGAAGTGCAGAGGCTGAGGCAATGGCTTTCTTGAAG 770
Db 421 GAAGAGCGAGTGGCTGCAAGTGAAGTGCAGAGGCTGAGGCAATGGCTTTCTTGAAG 480
QY 771 CAGCCCTTTAAGGATTTCTGACCAAGCTTCTAGCAAGTGCAGAGTGCAGAGTGC 830
Db 481 CAGCCCTTTAAGGATTTCTGACCAAGCTTCTAGCAAGTGCAGAGTGCAGAGTGC 540
QY 831 TTCGAGATGCAACCAAGTGTGAGCAAGTGTGAGTGCAGAGTGCAGAGTGCAGAGT 890
Db 541 TTCGAGATGCAACCAAGTGTGAGCAAGTGTGAGTGCAGAGTGCAGAGTGCAGAGT 600
QY 891 GGTTTTGGGAGGTATGTGCGCTCAGGTGAAAGTGCAGAGTGCAGAGTGCAGAGT 950
Db 601 GGTTTTGGGAGGTATGTGCGCTCAGGTGAAAGTGCAGAGTGCAGAGTGCAGAGT 660
QY 951 AAACCTGGACAGAGGCTGAGAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGT 1010
Db 661 AAACCTGGACAGAGGCTGAGAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGT 720
QY 1011 GAAATCTTGGAGAGGTGAGAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGT 1070
Db 721 GAAATCTTGGAGAGGTGAGAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGT 780
QY 1071 AAGACCCATCTCTGCTTGTGATGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGT 1130
Db 781 AAGACCCATCTCTGCTTGTGATGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGT 840
QY 1131 TACAAAGTGGGACGCGTGGCTGAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGT 1190
Db 841 TACAAAGTGGGACGCGTGGCTGAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGT 900
QY 1191 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGAGCATGAGCCTGAG 1250
Db 901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGAGCATGAGCCTGAG 960
QY 1251 AATGCTTCTGGATGACCTCGGCAACTGAGAGTGCAGAGTGCAGAGTGCAGAGT 1310
Db 961 AATGCTTCTGGATGACCTCGGCAACTGAGAGTGCAGAGTGCAGAGTGCAGAGT 1020
QY 1311 ATGAGGCTGGCAAGCCCATACCCAGAGG 1340
Db 1021 ATGAGGCTGGCAAGCCCATACCCAGAGG 1050
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RESULT 8

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US-10-217-745-3
; Sequence 3, Application US/10217745
; Patent No. 6838275
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilgenowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6838275el Human G-Coupled Protein Receptor Kinases and
; TITLE OF INVENTION: Polynucleotides
; TITLE OF INVENTION: Encoding the Same
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; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/10/217,745
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US/09/802,117
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: homo sapiens
; US-10-217-745-3
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Query Match 47.6%; Score 1046.8; DB 4; Length 1062;
Best Local Similarity 99.8%; Pred. No. 3.4e-258;
Matches 1048; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 291 ATGTGTGACATGGGGGCGCTGGACAACTGATGCCAACACCGCTACTTCCAGGCCCGG 350
Db 1 ATGTGTGACATGGGGGCGCTGGACAACTGATGCCAACACCGCTACTTCCAGGCCCGG 60
QY 351 AAGCCCTCGGACTCGACAGCAAGAGCTGCAGCGGCGGCGGTAGCTTGGCCCTGCCC 410
Db 61 AAGCCCTCGGACTCGACAGCAAGAGCTGCAGCGGCGGCGGTAGCTTGGCCCTGCCC 120
QY 411 GGGCTGCAGGGCTCGCGGAGCTCCGCCAGAGCTGTCCCTGAACTTCCACAGCCTGTGT 470
Db 121 GGGCTGCAGGGCTCGCGGAGCTCCGCCAGAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
QY 471 GAGCAGCGCCATCGGTGCGCGCTCTTCGTGACTTCTTAGCCACAGTGCACAGCTTC 530
Db 181 GAGCAGCGCCATCGGTGCGCGCTCTTCGTGACTTCTTAGCCACAGTGCACAGCTTC 240
QY 531 CGCAGGCGGCAACCTTCTTAGAGGACGTGAGAACTCGGAGCTGGCCGAGGAGGCC 590
Db 241 CGCAGGCGGCAACCTTCTTAGAGGACGTGAGAACTCGGAGCTGGCCGAGGAGGCC 300
QY 591 ACCAAGAAGCAGGCGCTGAGGGGTGTGGCCACTTGTGAGTGCCTTCCCGGGG 650
Db 301 ACCAAGAAGCAGGCGCTGAGGGGTGTGGCCACTTGTGAGTGCCTTCCCGGGG 360
QY 651 AAGCCGCAACCTTCTTAGCAGCAGCGCTTCTAGCAAGTGCAGAGTGCAGAGTGC 710
Db 361 AAGCCGCAACCTTCTTAGCAGCAGCGCTTCTAGCAAGTGCAGAGTGCAGAGTGC 420
QY 711 GAAGAGCGAGTGGCTGCAAGTGAAGTGCAGAGGCTGAGGCAATGGCTTTCTTGAAG 770
Db 421 GAAGAGCGAGTGGCTGCAAGTGAAGTGCAGAGGCTGAGGCAATGGCTTTCTTGAAG 480
QY 771 CAGCCCTTTAAGGATTTCTGACCAAGCTTCTAGCAAGTGCAGAGTGCAGAGTGC 830
Db 481 CAGCCCTTTAAGGATTTCTGACCAAGCTTCTAGCAAGTGCAGAGTGCAGAGTGC 540
QY 831 TTCGAGATGCAACCAAGTGTGAGCAAGTGTGAGTGCAGAGTGCAGAGTGCAGAGT 890
Db 541 TTCGAGATGCAACCAAGTGTGAGCAAGTGTGAGTGCAGAGTGCAGAGTGCAGAGT 600
QY 891 GGTTTTGGGAGGTATGTGCGCTCAGGTGAAAGTGCAGAGTGCAGAGTGCAGAGT 950
Db 601 GGTTTTGGGAGGTATGTGCGCTCAGGTGAAAGTGCAGAGTGCAGAGTGCAGAGT 660
QY 951 AAACCTGGACAGAGGCTGAGAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGT 1010
Db 661 AAACCTGGACAGAGGCTGAGAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGT 720
QY 1011 GAAATCTTGGAGAGGTGAGAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGT 1070
Db 721 GAAATCTTGGAGAGGTGAGAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGT 780
QY 1071 AAGACCCATCTCTGCTTGTGATGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGT 1130
Db 781 AAGACCCATCTCTGCTTGTGATGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGT 840
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QY 1131 TACAACTGGGACCGGTGGCTGACATGACCGGGTGTATCTTTTACTCGGCCAGATA 1190
DB 841 TACAACTGGGACCGGTGGCTGACATGACCGGGTGTATCTTTTACTCGGCCAGATA 900
QY 1191 GCCTGTGGGATGCTGCACCTCATGAATCGGCATGCTATATCGGGACATGAAGCTGAG 1250
DB 901 GCCTGTGGGATGCTGCACCTCATGAATCGGCATGCTATATCGGGACATGAAGCTGAG 960
QY 1251 AATGTCTTCTGGATGACCTCGGCAACTGACGTTTATCTGACCTGGGGTGGCGTGGAG 1310
DB 961 AATGTCTTCTGGATGACCTCGGCAACTGACGTTTATCTGACCTGGGGTGGCGTGGAG 1020
QY 1311 ATGAAGGTGGCAAGCCCATACCCAGAG 1340
DB 1021 ATGAAGGTGGCAAGCCCATACCCAGAG 1050

RESULT 9

US-09-738-894A-3
; Sequence 3, Application US/09738894A
; Patent No. 6331423
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000636
; CURRENT APPLICATION NUMBER: US/09/738,894A
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 36651
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(36651)
; OTHER INFORMATION: n = A,T,C or G
US-09-738-894A-3

Query Match 39.5%; Score 867.4; DB 3; Length 36651;
Best Local Similarity 95.1%; Pred. No. 1.9e-211;
Matches 895; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 1 GACCCCTAAGATGAAGGACCTCACTATAGGGCTCGAGCGCGCGCGCGAGGTGTTCCAGCAGCTTTC 60
DB 1786 GACCCCTAAGATGAAGGACCTCACTATAGGGCTCGAGCGCGCGCGCGAGGTGTTCCAGCAGCTTTC 1845
QY 61 GCCTTGGCAGGTGGGAGCATGACCTATCGTGTGACGTTCTTGGCGGGCTATACATAGCCA 120
DB 1846 GCCTTGGCAGGTGGGAGCATGACCTATCGTGTGACGTTCTTGGCGGGCTATACATAGCCA 1905
QY 121 GTCAAGGCTTTTACAAAGAAACCTTTTACACCTCCACGGGTGCCACCCACAGGCC 180
DB 1906 GTCAAGGCTTTTACAAAGAAACCTTTTACACCTCCACGGGTGCCACCCACAGGCC 1965
QY 181 ACAGGACTCACTGTAATCCCTTGGACGTTGTCTACCCGGGAAGGAAAGCAGCCAGCA 240
DB 1966 ACAGGACTCACTGTAATCCCTTGGACGTTGTCTACCCGGGAAGGAAAGCAGCCAGCA 2025
QY 241 GCCTTCCAGCCCTCTTGTGCTTTCTTGGAGTGGCGCGCGGTGCTCAGCCTATGGTGACA 300
DB 2026 GCCTTCCAGCCCTCTTGTGCTTTCTTGGAGTGGCGCGCGGTGCTCAGCCTATGGTGACA 2085
QY 301 TGGGGGCGCTTGACAACTGTATGCGCAACACCGCTTACCTGACGGCGCGGAAGCCCTCGG 360
DB 2086 TGGGGGCGCTTGACAACTGTATGCGCAACACCGCTTACCTGACGGCGCGGAAGCCCTCGG 2145
QY 361 ACTGCGACAGAAAGAGCTGACGGCGCGCGGTAGCTGCGCTGCGCCCTGCGCGGCTGCGAG 420
DB 2146 ACTGCGACAGAAAGAGCTGACGGCGCGCGGTAGCTGCGCTGCGCCCTGCGCGGCTGCGAG 2205

QY 421 GCTGGCGGAGTCCGCGCAGAGCTGTCCCTGAACCTTCCACAGCCTGTGTGAGCAGCAGC 480
DB 2206 GCTGGCGGAGTCCGCGCAGAGCTGTCCCTGAACCTTCCACAGCCTGTGTGAGCAGCAGC 2265
QY 481 CCATCGGTGCGCGCTCTTTCCGTGACTTCCCTAGCCACAGTGCACAGCTTCCGCAAGGCGG 540
DB 2266 CCATCGGTGCGCGCTCTTTCCGTGACTTCCCTAGCCACAGTGCACAGCTTCCGCAAGGCGG 2325
QY 541 CAACCTTCTAGAGGACGTGCAGAACTGGGAGCTGCGCGAGGAGGAGGCCACCAAGACA 600
DB 2326 CAACCTTCTAGAGGACGTGCAGAACTGGGAGCTGCGCGAGGAGGAGGCCACCAAGACA 2385
QY 601 GCGCGCTCAGGGGCTGTGCGCACTTGTGCGAGTGCCTCCCGGGGAAACCCGCAAC 660
DB 2386 GCGCGCTCAGGGGCTGTGCGCACTTGTGCGAGTGCCTCCCGGGGAAACCCGCAAC 2445
QY 661 CTTCTCCTCAGCCAGGCGCTGCGCACTTGTGCGAGTGCCTCCCGGGGAAACCCGCAAC 720
DB 2446 CTTCTCCTCAGCCAGGCGCTGCGCACTTGTGCGAGTGCCTCCCGGGGAAACCCGCAAC 2505
QY 721 TGGCTGACGTGACGCTGCGCAAGGCTGAGGCGCATGGCTTTTCTGCAAGAGCAGCCCTTTA 780
DB 2506 TGGCTGACGTGACGCTGCGCAAGGCTGAGGCGCATGGCTTTTCTGCAAGAGCAGCCCTTTA 2565
QY 781 AGGATTTCTGACACAGCGCTTCTTACGACAAAGTTTCTGAGTGGAACTCTTCGAGATGC 840
DB 2566 AGGATTTCTGACACAGCGCTTCTTACGACAAAGTTTCTGAGTGGAACTCTTCGAGATGC 2625
QY 841 AACCAGTGTGACAAAGTACTTCACTGAGTTCAGAGTCTGGGAAAGTGGTTTGGG 900
DB 2626 AACCAGTGTGACAAAGTACTTCACTGAGTTCAGAGTCTGGGAAAGTGGTTTGGG 2685
QY 901 AGGTATGTGCGCTCCAGCTGAAACACTGCGAAGATGTAT 941
DB 2686 AGGTATGTGCTCCAGTAGCCAGCTAGAAGTGAAGCAT 2726

RESULT 10

US-09-964-469-3
; Sequence 3, Application US/09964469
; Patent No. 6579709
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000636DIV
; CURRENT APPLICATION NUMBER: US/09/964,469
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 60/208,331
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: 09/738,894
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 36651
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(36651)
; OTHER INFORMATION: n = A,T,C or G
US-09-964-469-3

Query Match 39.5%; Score 867.4; DB 4; Length 36651;
Best Local Similarity 95.1%; Pred. No. 1.9e-211;
Matches 895; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 1 GACCCCTAAGATGAAGGACCTCACTATAGGGCTCGAGCGCGCGCGCGAGGTGTTCCAGCAGCTTTC 60
DB 1786 GACCCCTAAGATGAAGGACCTCACTATAGGGCTCGAGCGCGCGCGCGAGGTGTTCCAGCAGCTTTC 1845

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QY 61 GCCTGGCAGGTGGGAGCATGACCTATCGTGTGAGTTCCTGGCGGGCTATACATAGCCA 120
Db 1846 GCCTGGCAGGTGGGAGCATGACCTATCGTGTGAGTTCCTGGCGGGCTATACATAGCCA 1905
QY 121 GTCAAGAGCTTTTACAAAGAAACCTCTTTTACACCTTCCACGGGTCCACCCCAAGGCC 180
Db 1906 GTCAAGAGCTTTTACAAAGAAACCTCTTTTACACCTTCCACGGGTCCACCCCAAGGCC 1965
QY 181 ACAGAGCTCAGTGAATTCCTTGGAGCTTGTCTCACCCGGGAGGGAAGCAGCCAGCA 240
Db 1966 ACAGAGCTCAGTGAATTCCTTGGAGCTTGTCTCACCCGGGAGGGAAGCAGCCAGCA 2025
QY 241 GCCTTCCAGCCCTCTTGTGCTTTCCCTGGAGTGGCCCGCTGTCTACCCATGTTGGTGA 300
Db 2026 GCCTTCCAGCCCTCTTGTGCTTTCCCTGGAGTGGCCCGCTGTCTACCCATGTTGGTGA 2085
QY 301 TGGGGCCCTGGACAACTGATGCGCAACACCGCTTACTCTGAGGCCCGGAAGCCCTGG 360
Db 2086 TGGGGCCCTGGACAACTGATGCGCAACACCGCTTACTCTGAGGCCCGGAAGCCCTGG 2145
QY 361 ACTGGCAGCAGAAAGAGCTGACGGCGCGCGCTAGCTGCTGCGCGGCTGCGGCTGCA 420
Db 2146 ACTGGCAGCAGAAAGAGCTGACGGCGCGCGCTAGCTGCTGCGCGGCTGCGGCTGCA 2205
QY 421 GCTGGCGGAGCTCCGCCAGAACTGTCTCTGAACCTTCCACAGCTGTGTGAGCAGCAGC 480
Db 2206 GCTGGCGGAGCTCCGCCAGAACTGTCTCTGAACCTTCCACAGCTGTGTGAGCAGCAGC 2265
QY 481 CCATCGGTGGCGCTCTTCCGTGATCTTCTAGCCACAGTGCCCACTGCGCAAGGCGG 540
Db 2266 CCATCGGTGGCGCTCTTCCGTGATCTTCTAGCCACAGTGCCCACTGCGCAAGGCGG 2325
QY 541 CAACTTCTTAGAGAGCTGACAGAACTGGAGCTGGCGGAGGAGGACCCCAAGAGCA 600
Db 2326 CAACTTCTTAGAGAGCTGACAGAACTGGAGCTGGCGGAGGAGGACCCCAAGAGCA 2385
QY 601 GGGCGCTGAGGGGCTGTGGCCACTTGTGAGTGGCCCTGCGCGGGGAAACCGCAAC 660
Db 2386 GGGCGCTGAGGGGCTGTGGCCACTTGTGAGTGGCCCTGCGCGGGGAAACCGCAAC 2445
QY 661 CTTTCTCAGCAGCGCTGGCCACCAAGTGCCAAAGCAGCCACCTAGGAAGAGCGAG 720
Db 2446 CTTTCTCAGCAGCGCTGGCCACCAAGTGCCAAAGCAGCCACCTAGGAAGAGCGAG 2505
QY 721 TGGCTGAGTGAAGCTGCGCAGGCTGAGGCCATGCTTCTTCAAGCAGCAGCCCTTTA 780
Db 2506 TGGCTGAGTGAAGCTGCGCAGGCTGAGGCCATGCTTCTTCAAGCAGCAGCCCTTTA 2565
QY 781 AGGATTTCTGACAGCGCTTTTACGACAAAGTTTCTGAGTGGAACTCTTTCAGATGC 840
Db 2566 AGGATTTCTGACAGCGCTTTTACGACAAAGTTTCTGAGTGGAACTCTTTCAGATGC 2625
QY 841 AACAGTGTACAGAACTTCACTGATTCAGAGTGTGGGAAAGTGTGTTTGGGG 900
Db 2626 AACAGTGTACAGAACTTCACTGATTCAGAGTGTGGGAAAGTGTGTTTGGGG 2685
QY 901 AGGTATGTCCTTCAAGTGAAGAAACCTGGGAAGATGTAT 941
Db 2686 AGGTATGTCCTTCAAGTGAAGAAACCTGGGAAGATGTAT 2726
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RESULT 11

US-08-464-954A-2

; Sequence 2, Application US/08464954A

; Patent No. 625069

; GENERAL INFORMATION:

; APPLICANT: BENOVIC, JEFFREY L.; GOMEZ, JORGE; KINAPULI,

; APPLICANT: PRIYA

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR

; TITLE OF INVENTION: MODULATING THE ACTIVITY OF G PROTEIN-COUPLED RECEPTOR

; TITLE OF INVENTION: KINASES GRK5 AND GRK6

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

```
; ADDRESS: Jane Massey Licata, Esq.
; STREET: Woodland Falls Corporate Park
; STREET: 210 Lake Drive East, Suite 101
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,954A
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076,084
; FILING DATE: June 11, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: JEFF-0118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2848
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; ANTI-SENSE: NO
; US-08-464-954A-2
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Query Match 19.1%; Score 419.8; DB 3; Length 2848;

Best Local Similarity 56.2%; Pred. No. 3.1e-97;

Matches 891; Conservative 0; Mismatches 682; Indels 12; Gaps 5;

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QY 305 GGCCTGGACAACTGATCGCCAAACCGCTACTGTGAGCGCGCGGTAGCTGCGCGGCTGCAAG 364
Db 65 GGAGCTCGAAGCAATCGTAGCGAAACAGTCTACTCAAGGCCCGCGGAGGTGGCGTGG 124
QY 365 CGACGACAAAG---AGCTGACAGCGCGCGCGGTAGCTGCGCGGCTGCGCGGCTGCAAG 421
Db 125 AATCGCAAGCGCAAGCAAGAAATGCGCGCAGATGCTCCAGTTCCTCATCAGCA 184
QY 422 CTGCGCGAGCTCGCCAGAAAGCTGCTCCTGAACTTCCACAGCTGTGTGAGCAGCAGCC 481
Db 185 GTGCGAAGAGCTGGCGCTCAGCTCGAGCGTGAATATCAGAGCTGTGCGAGCGCACGC 244
QY 482 CATCGTGGCGCTCTTCCGTGACTTCTAGCCACAGTGCACAGTTCCTGCGCAAGCGCGC 541
Db 245 CATTTGGCGCTGTGTTCCGAGAGTCTGTGCGACAGAGCGCGAGCTGAGCGCTGGGT 304
QY 542 AACCTTCTAGAGCACTGGGAGCTGGCGAGCTGGCGAGGAGGAGCCCAAGAGAGCAG 601
Db 305 GCGCTTCTGATGGGTGGCGAGTGAATGATGATGATGATGATGATGATGATGATGATG 364
QY 602 CGCGCTGAGGGGCTGTGGCGCACTTGTGCGAGTGGCGCTGCGCGCGGGAACCCGCAACC 661
Db 365 TGGCGGCGACG---TAACGCGAATTTTCTGAGCCACACGCGGTCTCTGACCTCATCCTGA 421
QY 662 CTTCTCAGCCAGCGCGTGGCGCAAGTGCACAGCAGCCACCTAGTAGGAAGAGCGAGT 721
Db 422 GGTCCCGCGCAGCTGTGTGAGCAAC-TGACCCCGCGCTGAGCAGAGGTCTCTGCAAG 480
QY 722 GCGTCACTGAGCTGCGCAAGAGGTGAGCCATGCTTTTCTTTCAGAGCAGCAGCCCTTAA 781
Db 481 ACCTTTCCAGGAAGTCAACCGGCTGA---CCACGAGTACCTGAGCGTGGCGCTTTGC 538
QY 782 GGATTTCTGAGCCAGCGCTTCTAGCAAGTCTTCTGAGTGGAAACTCTTTCAGATGCA 841
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Db 539 CGACTACCTCGACAGCATCTTCAACCGTTTCTCTGAGTGAAGTGGCTGGAAAGGCA 598
QY 842 ACCAGTGTGACAGATGATCTTCACTGAGTTCAGAGTGTGGGGAAAGGTGGTGGGA 901
Db 599 GCGAGTACCAAAACACCTCTCAGGCAATACCGAGTCTCTGGGCAAGGTGGCTGGGA 658
QY 902 GGTATGTGCGTCCAGTGAAGAAACACTCGGAGATGTATGCTGTGAAGAACTGGACA 961
Db 659 GGTGTGCGCTCGCAGTGTGGGGCCACAGGTAGATGTATGCTGTGAAGAACTGGACA 718
QY 962 GAAGCGGCTGAAGAAAGGTGGGAGAGATGGCTCTCTTGGAAAGGAAATCTTGA 1021
Db 719 AAAGCGGATCAAGAGCGGAAGGGAGGCCATGGCGCTGAAGAGAGCAGATCTTGA 778
QY 1022 GAAGTACAGACGCTTTTCAATGTCTCTGTGCGCTATGCTTTGAGAGCAAGACCATCT 1081
Db 779 GAAAGTGAACAGTAGTGTGTAGTGAAGTGTGGCTTACGCTATGAGACCAAGGACGCT 838
QY 1082 CTGCGCTTGTATGAGCTGATGAATGGGGAGACCTCAAGTTCACATCTACAACTGGG 1141
Db 839 GTGCTGTGTGACACTGATGAACGGGGGCGACCTCAAGTTCACATCTACCAATGGG 898
QY 1142 CACGCGTGGCTCGGACATGAGCGGGGTGATCTTTTACTCGGCCAGATAGCCTGTGGAT 1201
Db 899 CCAGCTGGCTTCCCGAAGCGGGCGCTCTTCTACGCGCGGAGATCTGTGTGGCT 958
QY 1202 GGTGACCTTCAAGAACTCGGATCGTCTATCGGACATGAAGCTGAGAAATGTCTTCT 1261
Db 959 GGAGGACCTGCACCGGGAGCGCATCGTGTACAGGAGCCTGAAGCCGAGAACATCTTGT 1018
QY 1262 GGATGACCTCGCACTGAGGTTATCTGACCTGGGGTGGCGGTGGAGTGAAGGGTGG 1321
Db 1019 GGATGACCACGGCCATCTCGCATCTCTGACCTGGGACTAGCTGTGCTGCGCGAGG 1078
QY 1322 CAAGGCCATCACCCAGAGGGCTGGAACCAATGTTTACATGGCTCTGAGATCCTAATGA 1381
Db 1079 CCAGACCAATCAAGGGCGTGTGGGACCGTGGGTATCATGGCTCCGGAG---GTGGTGA 1135
QY 1382 AAGTGAAGTTATCTCTCTGTGGACTGTTTGGCATGGGATGAGCATTTATGAAT 1441
Db 1136 GAATGAACGGTACAGCTTCAGCGCTGACTGTGGGGCTCGGCTGCTCTGTACGAT 1195
QY 1442 GTTGTGACGACCAACCATTTCAAGATTAACAGGAAAGGTGAGTGAAGGATCTGA 1501
Db 1196 GATCAGCGCCAGTGCCTTCCAGCAGAGGAAGAAAGATCAAGCGGGAGGAGGTGA 1255
QY 1502 GCAAGAACTCTGCAAGAGAGGTCAAAATCCAGCATGATTAATTCACAGAGGAAGCAA 1561
Db 1256 GCGGCTGTGAAGAGGTCCCGAGAGTATTCGAGCGGTTTTCCCGAGCGCGCTC 1315
QY 1562 AGATATTTGAGGCTCTTCTTGGCTTAAGAAACAGAGCAACGCTTTAGGAAGCAGAGAAA 1621
Db 1316 ACTTGTCTCACAGCTCTCTGCAAGGACCCCTGCGNACGCTGGGGTGTGTGGGGCAG 1375
QY 1622 GTCTGATGATCCAGGAAACATATTTCTTTAAACGATCAACTTTCTGCTGCTGGAAGC 1681
Db 1376 TGCCCGGAGGTGAAGAGGACCCCTCTTTAAGAAAGTGAATTTCAAGCGGCTGGAGC 1435
QY 1682 TGGCTTAATGAACCCCAATTTGTGCGAGACCTTTCAGTGGTTTATGCAAGACATCGC 1741
Db 1436 TGGCATGTGGAGCGCGCTTCAAGCCTGACCCCGAGGCAATTTACTGCAAGGATGTCT 1495
QY 1742 TGAATTTGATTTCTCTGAGGTTCTGGGGGTGGAATTTGATGACAAAGATAAGCAGTT 1801
Db 1496 GGACATTGACAGTTCTCTACGTTCAAGGGCGTGGAGCTGAGCCCTACCGACAGCAGTT 1555
QY 1802 CTTCAAAACCTTTGCGACAGGTGCTTCTTATAGCATGGCAGGAAGAAATTTATGAAC 1861
Db 1556 CTCACCAAGATTTGCGACAGGAGGTGCGCCATCCCTTGGCAGACGAGATGTTGGAGAC 1615
QY 1862 GGGACTGTTTGGGAACTGAATGAC 1886
Db 1616 CGAGTGTTCGAAGAGCTGAATGTC 1640

RESULT 12

US-08-221-817-12
; Sequence 12, Application US/08221817
; Patent No. 5532151
; GENERAL INFORMATION:
; APPLICANT: Chantry, David
; APPLICANT: Gray, Patrick W.
; APPLICANT: Hoekstra, Merle F.
; TITLE OF INVENTION: A No. 5532151el G Protein-Coupled Receptor
; TITLE OF INVENTION: Kinase GRK6
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESS: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,817
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/123,932
; FILING DATE: 17 SEP 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5532151and, Greta B.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31981
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2204 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31..1758
US-08-221-817-12

Query Match 19.0%; Score 418.2; DB 1; Length 2204;
Best Local Similarity 56.2%; Pred. No. 7.1e-97;
Matches 890; Conservative 0; Mismatches 683; Indels 12; Gaps 5;

QY 305 GGCCTTGACAACTGATCGCAACACACCGCTACTCTGAGCGCCGGAAGCCTCGGACTG 364
Db 33 GGAGCTCGAAGCAATCGTAGCAACACGCTGCTACTCAAGGCCCGGAGGTGGCGGTGG 92
QY 365 CGACGACAAAG---AGCTGACGCGCGCGGCTAGCCTGGCGCTGCGGCTGACAGG 421
Db 93 AAATCGCAAGGCAAGAAATGGCGCAGATGCTCCAGTTTCCCTCACATCAGCA 152
QY 422 CTGCGCGAGCTCGCCGAGAGCTGTCTCCGAACTTCCACAGCTGTGTGAGCAGCACC 481
Db 153 GTGCGAAGAGCTGGGGCTCAGCTCGAGCGTGAATATCACAGCTGTGCGAGCGGACCG 212
QY 482 CATGGTGGCGGCTCTTCCGTGACTTCCAGCAGCAGTGGCCAGCTTCCGCAAGGCGGC 541
Db 213 CATTGGGCGGCTGCTGTTCGAGAGTCTGTGTCACAGGCGCGAGCTGAGCGCTGCGT 272

QY 542 AACCTTCTAGAGGACGTGCGAAGCTGGAGCTGGCCGAGGAGGACCCACCAAGACAG 601
Db 273 CGCCTTCTCGATGGGTGGCGAGTATGAAGTGAAGCCCGGATCAAGCGGAAGCATG 332
QY 602 CGCGCTGAGGGGCTGGTGGCACTTGTGCGAGTGCCTCCCGGGGAACCCGCAACC 661
Db 333 TGGCGGGACG---TAACGAGAAATTTTCTGAGCCACACGCGGTCTGACCTCATCCCTGA 389
QY 662 TTCTCTCAGCCAGCGCGTGGCCACCAAGTGCCCAAGCAGCCACCACTGAGGAAGAGCGAGT 721
Db 390 GGTCCCCCGGACGTGGTGAAGAAC-TGACCCAGCGGTGAGGAGAGGTCCCTGCAAG 448
QY 722 GCGTGCAGTGCCTGCGCAAGCTGAGGCCATGCTTTCTTGCAGAGCAGCCCTTTAA 781
Db 449 ACCTTTTCCAGGAATCAACCGGCTGA--CCACAGTACCTGAGCGTGGCCCTTTTCG 506
QY 782 GGAATTCGTGACAGCGCTTCTAGCAAGTTTCTGCAAGTGGAAATCTTTCGAGATGA 841
Db 507 CGATACCTCGACAGCATCTACTTCAACCGTTTCTGCAAGTGAAGTGGCTGGAAGGCA 566
QY 842 ACCAGTGTGACAGCAAGTACTTCACTGAGTTCAAGTGTGCGGAAAGGTGTTTGGGA 901
Db 567 GCAGTGACCAAAACACCTTCAGCAATACCGAGTCTTGGTAAAGTGGCTTTGGGA 626
QY 902 GGTATGTGCGCTCCAGGTGAAACCACTGGGAAGATGTATGCTCTGAAGAACTGGACAA 961
Db 627 GGTGTGCGCTCCAGGTGCGGGCCACAGGTAAAGATGTATGCTTCAAGNAGCTAGAGAA 686
QY 962 GAAGCGGTGAAGAAAGGTGGCGAGAGATGCTCTTCTTGGAAAGAAATCTTGA 1021
Db 687 AAAGCGGATCAAGAAAGCGGAAAGGGAGGCCATGCGCTGAACGAGAAAGCAGATCCTGA 746
QY 1022 GAAGGTGACAGCCCTTTCATTTCTCTGCTGCTATGCTTTGAGAGCAAGACCATCT 1081
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QY 1082 CTGCTTGTGATGAGCTGATGAATGGGGAGACCTCAAGTTTCCACATCTACAAGCTGG 1141
Db 807 GTGCTGTGCTGACACTGATGAACGGGGCGACCTCAAGTTTCCACATCTACCACATGG 866
QY 1142 CAGCGTGGCTGGACATGAGCGGGTGATCTTTTACTGGCCAGATAGCTTGGGAT 1201
Db 867 CCAGCTGGCTTCCCGAAGCGCGGCGCTCTTCTACGCGCGAGATCTGCTGGGCT 926
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QY 1262 GATGACCTTCGCAACTGCGAGTTATCTGACCTGGGGTGGCGGTGAGATGAAGGGTG 1321
Db 987 GATGACCAAGCCACATCGCATCTCTGACCTGGGACTAGCTGTGATGTGCCGAGGG 1046
QY 1322 CAGGCCATACCCAGAGGCTGGAACCAATGGTTACATGGCTCTGAGATCTTAATGA 1381
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QY 1382 AAGGTAGTATTCTTCTCTGTGCTGCTGTTTCCATGGATGAGCATTTAGTAAT 1441
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QY 1442 GGTGTGTCGACGAACACCATTCACAAAGATTTACAGGAAAGGTTCAGTAAGAGGATCTGAA 1501
Db 1164 GATCGAGGCGAGTCGCCCTTCCAGCAGAGGAGGAGAGATCAAGCGGAGGAGGTGA 1223
QY 1502 GCAAGAACTCTGCAAGAGAGGTCAATTCAGCATGATTAATCTTACAGAGGAAGCAAA 1561
Db 1224 GCGGCTGTGAAGAGGTCCTCCGAGGAGTATTCGAGGCGCTTTCCCGCGAGCCGCTC 1283
QY 1562 AGATATTGAGGCTTCTTGGCTTAAGAAACACAGCAACGCTTAGNAGCAGAGAA 1621
Db 1284 ACTTGTCTACAGCTCTCTTGAAGGACCTTCCGAGCCCTGGGGGTGCTGGGGGCGAG 1343
QY 1622 GTCTGATGATCCAGGAAACATCAATTTCTTTAAACGATCAACTTTCTCTCGCTGGAAGC 1681

Db 1344 TGCCCGGAGGTGAAGGAGCACCCCTCTTTAAAGAGCTGAACCTCAAGCGGCTGGGAGC 1403
QY 1682 TGGCTTAATTCAAACCCCATTTGTGCCAGACCCCTTCAGTGGTTTATGCAAGACATCGC 1741
Db 1404 TGGCATGTGAGCGCGCGTTCAAGCCCTGACCCCGAGCCATTTACTCAAGGATGTTCT 1463
QY 1742 TGAATATGATGATTTCTGAGGTTCCGGGGGTGGAATTTGATGACAAAGATAAGCAGTT 1801
Db 1464 GGACATTGAACAGTTCTTACGGTCAAGGGCGTGGAGCTGAGCCTACCGACGAGCTT 1523
QY 1802 CTTCAAAACCTTTGGCAGAGTGTCTTCTATAGCATGGCAGGAAGAAATATAGAAAC 1861
Db 1524 CTACAGAAAGTTTGCACAGGACGTGTGCCCATCCCTGGCAGAACGAGATGTTGGAGAC 1583
QY 1862 GGGACTGTTTGGAGAACTGATGAC 1886
Db 1584 CGAGTGCTTCCAAGAGCTGAATGTC 1608

RESULT 13

US-08-454-439-12
; Sequence 12, Application US/08454439
; Patent No. 5591618
; GENERAL INFORMATION:
; APPLICANT: Chantry, David
; APPLICANT: Gray, Patrick W.
; APPLICANT: Hoekstra, Merle F.
; TITLE OF INVENTION: A No. 5591618el G Protein-Coupled Receptor
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,439
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,817
; FILING DATE: 31-MAR-1994
; APPLICATION NUMBER: 08/123,932
; FILING DATE: 17 SEP 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5591618and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31981
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2204 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31..1758
US-08-454-439-12

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Db	33	GGAGCTCGAACAATCTGTAGGAACACGGTGTACTCAAGGCCCGGGAAGGTGCGGTGG	92	
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PCT-US94-10487-12
; Sequence 12, Application PC/TUS9410487
; GENERAL INFORMATION:
; APPLICANT: ICOS Corporation
; TITLE OF INVENTION: A Novel G Protein-Coupled Receptor
; TITLE OF INVENTION: Kinase GRK6
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10487
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/221,817
; FILING DATE: 31 MAR 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/123,932
; FILING DATE: 17 SEP 1993

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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/31981
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2204 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 31..1758
PCT-US94-10487-12

Query Match 19.0%; Score 418.2; DB 5; Length 2204;
Best Local Similarity 56.2%; Pred. No. 7.1e-97;
Matches 890; Conservative 0; Mismatches 683; Indels 12; Gaps 5;
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DB 33 GGAGCTCGAGACATCGTAGCGNACACGGTGTCTCAAGGCCCGGGAGGTGGCGTGG 92
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QY 422 CTGGCGGAGCTCCGCCAAGCTGTCCCTGAACTTCCACAGCTGTGTGACGACGCC 481
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; Sequence 21 Application US/08221817
; Patent No. 5532151
; GENERAL INFORMATION:
; APPLICANT: Chantry, David
; APPLICANT: Gray, Patrick W.
; APPLICANT: Hoeftstra, Merle F.
; TITLE OF INVENTION: A No. 5532151e1 G Protein-Coupled Receptor
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:

QY 1862 GGGACTGTTTGAGGAACGAATGAC 1886
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Db 1566 TGAGTCTTCCAGGAACGAATGTC 1590

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 11, 2005, 00:07:33 ; Search time 2882.42 Seconds
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Listing first 45 summaries

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22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2008.8	91.4	2249	9 US-09-802-117-5	Sequence 5, Appli
3	2008.8	91.4	2249	14 US-10-217-745-3	Sequence 5, Appli
4	1659	75.5	1659	13 US-10-044-205A-3	Sequence 3, Appli
5	1658.8	75.5	1662	17 US-10-311-034-45	Sequence 45, Appl
6	1658.8	75.5	1662	17 US-10-451-168-49	Sequence 49, Appl
7	1658.8	75.5	1662	19 US-10-788-197-22	Sequence 22, Appl
8	1658.4	75.5	1662	9 US-09-802-117-1	Sequence 1, Appli
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18	423	19.2	1770	19 US-10-788-197-6	Sequence 10, Appli
19	418.2	19.0	2848	19 US-10-788-197-10	Sequence 2, Appli
20	418.2	19.0	2848	9 US-09-851-686-2	Sequence 4, Appli
21	418.2	19.0	2848	10 US-09-873-367C-142	Sequence 142, App
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23	418.2	19.0	2848	19 US-10-843-641A-142	Sequence 24, Appl
24	407.4	18.5	1692	19 US-10-788-197-24	Sequence 621, App
25	401.6	18.3	2817	17 US-10-388-934-621	Sequence 110, App
26	379.4	17.3	2467	15 US-10-084-817-110	Sequence 12, Appl
27	377.8	17.2	1773	19 US-10-788-197-12	Sequence 13, Appl
28	377.8	17.2	2519	13 US-10-071-766-13	Sequence 72, Appl
29	374.6	17.0	2519	10 US-09-971-392-72	Sequence 60, Appl
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45	311.6	14.2	1503	19 US-10-788-197-14	

ALIGNMENTS

RESULT 1
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; Sequence 1, Application US/10044205A
; Publication No. US20020123464A1
; GENERAL INFORMATION:
; APPLICANT: KAPPELLER-LIBERMANN, Rosana
; APPLICANT: BANDARU, Rajasekhar
; TITLE OF INVENTION: 65087, 15821, and 15418, Methods and Compositions of Human Protei
; FILE REFERENCE: 10147-52U1
; CURRENT FILING DATE: 2002-04-19
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US/10/044,205A
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: US 60/242,428
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: US 60/241,884
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/241,877
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2198
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-044-205A-1

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1081 TCTGCTTGTATGACCTGTATGAATGGGGAGACCTCAAGTTCACATCTACAACTGG 1140
QY 1141 GCACGGTGGCCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCGAGATAGCCTGTGGGA 1200

DB 1141 GCACGGTGGCCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCGAGATAGCCTGTGGGA 1200
QY 1201 TGCTGCACCTCATGAACCTCGGCATCGTCTATCGGGAATGAAGCCTGAGAAATGTCTTC 1260
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QY 1261 TGGATGACCTCGGCAACTGCAAGTTATCTGACCTCGGCGTGGCGTGGAGATGAAGGGTG 1320
DB 1261 TGGATGACCTCGGCAACTGCAAGTTATCTGACCTCGGCGTGGCGTGGAGATGAAGGGTG 1320
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DB 1321 GCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAGATCTTAATGG 1380
QY 1381 AAAAGGTAAATTTCTATCTCTGATCTGGTTCATGGATGCAAGCAATTAAGAAA 1440
DB 1381 AAAAGGTAAATTTCTATCTCTGATCTGGTTCATGGATGCAAGCAATTAAGAAA 1440
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DB 1561 AAGATATTTGACGCTCTTCTTGGCTAAGAAACAGAGCAACGCTTAGGAAGCAGAGAAA 1620
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DB 1621 AGTCTGATGATCCAGAGAAACATCATTTCTTTAAACGATCAACTTCTCGCTCGGAG 1680
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DB 1681 CTGCGCTAAATTTGAACCCCAATTTGTGCCAGACCTTTCAGTGGTTTATGCCAAAGACATCG 1740
QY 1741 CTGAAATTTGATGATTTCTCTGAGTTTGGGGGGTGGAAATTTGATGACAAAGATAGCAGT 1800
DB 1741 CTGAAATTTGATGATTTCTCTGAGTTTGGGGGGTGGAAATTTGATGACAAAGATAGCAGT 1800
QY 1801 TCTTCAAAAACCTTTGCCAGAGTCTGCTCTATAGCATGGCAGGAAAGAAATATAGAAA 1860
DB 1801 TCTTCAAAAACCTTTGCCAGAGTCTGCTCTATAGCATGGCAGGAAAGAAATATAGAAA 1860
QY 1861 CGGACCTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTGTGTGAGGGGTAAAT 1920
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QY 1921 CATCCAGTCTGGCGTGTGTTTGTATTTATTAATTTGCTCTTTTACAGACAGGACGAG 1980
DB 1921 CATCCAGTCTGGCGTGTGTTTGTATTTATTAATTTGCTCTCTTTTACAGACAGGACGAG 1980
QY 1981 GAGTCTCGGCTGACATAATCTCGAATGTTTCCACAGCTGGAATCTCTGGAATGAGGCT 2040
DB 1981 GAGTCTCGGCTGACATAATCTCGAATGTTTCCACAGCTGGAATCTCTGGAATGAGGCT 2040
QY 2041 AATCAGTTAGGAGGACATCAACCAAAACAAATTTCAAAAGACAGGCAAGCTCACTAC 2100
DB 2041 AATCAGTTAGGAGGACATCAACCAAAACAAATTTCAAAAGACAGGCAAGCTCACTAC 2100
QY 2101 TAGAACACATTTTATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 2160
DB 2101 TAGAACACATTTTATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 2160
QY 2161 CTGAGGCGAGGAAAGGAAACACTCAGGTTTATTTTGA 2198
DB 2161 CTGAGGCGAGGAAAGGAAACACTCAGGTTTATTTTGA 2198

US-09-802-117-5									
; Sequence S, Application US/09802117									
; Publication NO. US20020042503A1									
; GENERAL INFORMATION:									
; APPLICANT: Walke, D. Wade									
; APPLICANT: Wilganowski, Nathaniel L.									
; APPLICANT: Turner, C. Alexander Jr.									
; TITLE OF INVENTION: No. 644456el Human G-Coupled Protein Receptor Kinases and Polynu									
; FILE REFERENCE: Encoding the Same									
; CURRENT APPLICATION NUMBER: US/09/802,117									
; CURRENT FILING DATE: 2001-03-08									
; PRIOR APPLICATION NUMBER: US 60/188,449									
; PRIOR FILING DATE: 2000-03-10									
; NUMBER OF SEQ ID NOS: 5									
; SOFTWARE: FastSeq for Windows Version 4.0									
; SEQ ID NO 5									
; LENGTH: 2249									
; TYPE: DNA									
; ORGANISM: homo sapiens									
US-09-802-117-5									
Query Match 91.4%; Score 2008.8; DB 9; Length 2249;									
Best Local Similarity 99.9%; Pred. No. 0; Mismatches 2; Indels 0; Gaps 0;									
Matches 2010; Conservative 0; Gaps 0;									
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Qy	235	CAGCAGCCCTCAGCCCTCTTGTGCTTTCCTTGGAGTGCCTCCCTGCTCAGCCATGG	294						
Db	298	CAGCAGCCCTCAGCCCTCTTGTGCTTTCCTTGGAGTGCCTCCCTGCTCAGCCATGG	357						
Qy	295	TGGACATGGGGCCCTGGACACCTGTGTCACACCGCCCTACCTGCAGGCCCGGAAGC	354						
Db	358	TGGACATGGGGCCCTGGACACCTGTGTCACACCGCCCTACCTGCAGGCCCGGAAGC	417						
Qy	355	CCTCGGACTGCACAGCAAGAGCTGCAGCGCGCGGGTGCCTGAGCCTGCGCCGGGC	414						
Db	418	CCTCGGACTGCACAGCAAGAGCTGCAGCGCGCGGGTGCCTGAGCCTGCGCCGGGC	477						
Qy	415	TGCAGGCTGCGGAGCTCCGCCAAGAGCTGTCTCCTGAACTTTCACAGCCTGTGTGAGC	474						
Db	478	TGCAGGCTGCGGAGCTCCGCCAAGAGCTGTCTCCTGAACTTTCACAGCCTGTGTGAGC	537						
Qy	475	AGCAGCCATCGTGCAGCCCTCTTCCGTAAGCTTCTTACCCACAGTGCCTCCCGCA	534						
Db	538	AGCAGCCATCGTGCAGCCCTCTTCCGTAAGCTTCTTACCCACAGTGCCTCCCGCA	597						
Qy	535	AGGCGGCAACCTTCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGACCCACCA	594						
Db	598	AGGCGGCAACCTTCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGACCCACCA	657						
Qy	595	AAGCAGCGCTGCAGGCGCTGGTGCCACCTTGTGAGTGCCTTGCAGTGCCTGCGGGAAAC	654						
Db	658	AAGCAGCGCTGCAGGCGCTGGTGCCACCTTGTGAGTGCCTTGCAGTGCCTGCGGGAAAC	717						
Qy	655	CGCACCCTTCTCAGCCAGCGCTGGCCACCAAGTGCACAGCCACCACTGAGGAAG	714						
Db	718	CGCACCCTTCTCAGCCAGCGCTGGCCACCAAGTGCACAGCCACCACTGAGGAAG	777						
Qy	715	AGCAGTGGCTCAGTGCAGCTGCGCAAGGCTGAGGCCATGCTTCTTGCAGAGCAGC	774						
Db	778	AGCAGTGGCTCAGTGCAGCTGCGCCAGGCTGAGGCCATGCTTCTTGCAGAGCAGC	837						
Qy	775	CTTTAAGATTTCGACAGCGCTTCTACCAAGTTTCTCAGTGGAACTCTTGG	834						
Db	838	CTTTAAGATTTCGACAGCGCTTCTACCAAGTTTCTCAGTGGAACTCTTGG	897						
Qy	835	AGATCCACCAAGTTCAGACAAAGTACTCAGTTCAGATGCTGGGAAAGTGGTT	894						
Db	898	AGATCCACCAAGTTCAGACAAAGTACTCAGTTCAGATGCTGGGAAAGTGGTT	957						

Qy	895	TTGGGAGGTATGTCCGCTCCAGGTGAAAAACA	954						
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Qy	955	TGGCAAGAACGGCTGAAGAGAGGTGGCGAGAGATGCTCTCTTTGGAAAGGAAA	1014						
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Qy	1015	TCTTGGAGAAAGTCAAGCAGCCCTTTTCAATGTCTCTCTGCGCTATGCTTTTGAGAGCAAGA	1074						
Db	1078	TCTTGGAGAAAGTCAAGCAGCCCTTTTCAATGTCTCTCTGCGCTATGCTTTTGAGAGCAAGA	1137						
Qy	1075	CCCATCTCTGCTTCTCATGAGCCCTGATGAATGGGGAGACCTCAAGTTCCACATCTACA	1134						
Db	1138	CCCATCTCTGCTTCTCATGAGCCCTGATGAATGGGGAGACCTCAAGTTCCACATCTACA	1197						
Qy	1135	AGTGGGCAAGCGCTGGACATGAGCGGGTGTCTTTTACTCGGCCCCAGATAGCCT	1194						
Db	1198	AGTGGGCAAGCGCTGGACATGAGCGGGTGTCTTTTACTCGGCCCCAGATAGCCT	1257						
Qy	1195	GTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGACATGAAGCCTGAGAAATG	1254						
Db	1258	GTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGACATGAAGCCTGAGAAATG	1317						
Qy	1255	TGCTTCTGATGACCTCGGCCAACTGCAGGTTATCTGACCTGGGGTGGCGCTGGAGATGA	1314						
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Qy	1315	AGGTGGCAAGCCCATCAAGAGGGCTGGACCAATGGTTTACATGGCTCTGTAGATCC	1374						
Db	1378	AGGTGGCAAGCCCATCAAGAGGGCTGGACCAATGGTTTACATGGCTCTGTAGATCC	1437						
Qy	1375	TAATGAAAAGTAAAGTTATTTCTCTATCTGTGACCTGGTTTGCATGGATGAGCATTT	1434						
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Qy	1435	ATGAAATGGTTGCTGGACGAAACACCATTTCAAAGATTACAAGAAAAGGTTCAGTAAAGAGG	1494						
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Qy	1495	ATCTGAACAAAGAACTCTGCAAGCAGAGGTCAAAATTCAGCATGATTAATTCACAGAGG	1554						
Db	1558	ATCTGAACAAAGAACTCTGCAAGCAGAGGTCAAAATTCAGCATGATTAATTCACAGAGG	1617						
Qy	1555	AAGCAAAAGATATTTGACAGGCTCTTCTTGGCTTAAGAAAACAGACAAACGCTTTAGGAAGCA	1614						
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Qy	1615	GAGAAAAGTCTGATGATCCAGGAAACATCATTTCTTTAAACACGATCAACTTTCTCGCC	1674						
Db	1678	GAGAAAAGTCTGATGATCCAGGAAACATCATTTCTTTAAACACGATCAACTTTCTCGCC	1737						
Qy	1675	TGGAAGCTGGCTTAATTTGAACCCCATTTTGGCCAGACCTTCAGTGGTTATGCGCAAG	1734						
Db	1738	TGGAAGCTGGCTTAATTTGAACCCCATTTTGGCCAGACCTTCAGTGGTTATGCGCAAG	1797						
Qy	1735	ACATCGCTGAAATGATGATTTCTGAGGTTTGGGGGTGGAAATTTGATGACAAAGATA	1794						
Db	1798	ACATCGCTGAAATGATGATTTCTGAGGTTTGGGGGTGGAAATTTGATGACAAAGATA	1857						
Qy	1795	AGCAGTTCTTCAAAAACCTTGGCAGAGGTGTGTTTCTTATAGCATGGCAGGAGAAATTA	1854						
Db	1858	AGCAGTTCTTCAAAAACCTTGGCAGAGGTGTGTTTCTTATAGCATGGCAGGAGAAATTA	1917						
Qy	1855	TAGAAAACGGGACTGTTTGAAGGAACTGAATGACCCCAACAGACCTACGGGTGTGAGGAGG	1914						
Db	1918	TAGAAAACGGGACTGTTTGAAGGAACTGAATGACCCCAACAGACCTACGGGTGTGAGGAGG	1977						
Qy	1915	GTAATTCACCAAGTCTGCGCTGTGTTGTTATTTGTAATTCGCTCTCTTTACACAGCAGG	1974						
Db	1978	GTAATTCACCAAGTCTGCGCTGTGTTGTTATTTGTAATTCGCTCTCTTTACACAGCAGG	2037						


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Db 1738 TGAAGCTGGCCATAATGAACCCCATTTGTGCCAGACCCCTTCAGTGGTTTATGCCAAAG 1797
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Qy 1795 AGCAGTTCTTCAAAAACCTTTGGGACAGGTGCTGTTTCCTATAGCATGGGAGGAAAGATA 1854
Db 1858 AGCAGTTCTTCAAAAACCTTTGGGACAGGTGCTGTTTCCTATAGCATGGGAGGAAAGATA 1917
Qy 1855 TAGAAACGGGACTGTTTGGAGAACTGAATGACCCCAACAGACCTACGGGTTGTGAGGAGG 1914
Db 1918 TAGAAACGGGACTGTTTGGAGAACTGAATGACCCCAACAGACCTACGGGTTGTGAGGAGG 1977
Qy 1915 GTAATTCATCCAGTCTGGCTGTGTTTGTATTTGTAATTTGCTCTCTTTTACCAGACAGG 1974
Db 1978 GTAATTCATCCAGTCTGGCTGTGTTTGTATTTGTAATTTGCTCTCTTTTACCAGACAGG 2037
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Db 2038 CAGCAGGAGTCTGGCTGACATAATCTCGAATGTTTCCACAGCTGGAATCTGTGGAATG 2097
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Db 2098 AGGGCTAATCAGTTAGGAGGACATCAACACACAAACNATTTCAAAGACAGGCAAGCT 2157
Qy 2095 CACTACTAGAACACATTTTATTTTCTTTTCTTTCTTCTATAAAGATGAGTAAAGTCTCAG 2154
Db 2158 CACTACTAGAACACATTTTATTTTCTTTTCTTTCTTCTTCTTCTTCTTCTTCTTCTCAG 2217
Qy 2155 TTTTTCACGTGAGGCGAGGAAAGGAACACTCA 2186
Db 2218 TTTTTCACGTGAGGCGAGGAAAGGAACACTCA 2249

RESULT 4
US-10-044-205A-3
; Sequence 3, Application US/10044205A
; Publication No. US20020123464A1
; GENERAL INFORMATION:
; APPLICANT: KAPILLER-LIBERMANN, Rosana
; APPLICANT: BANDARU, Rajasekhar
; TITLE OF INVENTION: 69087, 15821, and 15418, Methods and Compositions of Human Protei
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 10147-52U1
; CURRENT APPLICATION NUMBER: US/10/044,205A
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/242,428
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: US 60/241,884
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/241,877
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1659
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-044-205A-3

Query Match 75.5%; Score 1659; DB 13; Length 1659;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1659; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 291 ATGTTGACATGGGGGCTTGACAACTGATTCGCAACACCGCTTACTGACGGCCCG 350
Db 1 ATGTTGACATGGGGGCTTGACAACTGATTCGCAACACCGCTTACTGACGGCCCG 60

Qy 351 AAGCCCTCGGACTGCGACAGCAAGAGCTGACGGCGCGCGCTAGGCTGGCCCTGCC 410
Db 61 AAGCCCTCGGACTGCGACAGCAAGAGCTGACGGCGCGCGCTAGGCTGGCCCTGCC 120
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Qy 411 GGGCTGCAGGCGTGGCGGGAGCTCGCCAGAAAGCTGTCCCTGAACTTCCACAGCCTGTGT 470
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Qy 471 GAGCAGCAGCCCATCGGTCCGGCGCTCTTCGCTGACTTCCAGTCCACAGTCCCAAGTTC 530
Db 181 GAGCAGCAGCCCATCGGTCCGGCGCTCTTCGCTGACTTCCAGTCCACAGTTCGCCACGTTT 240
Qy 531 CGCAAGCGCGCAACCTTCTTAGAGGACGTGCAGAACTGGGAGCTGGCGAGGAGGAGCC 590
Db 241 CGCAAGCGCGCAACCTTCTTAGAGGACGTGCAGAACTGGGAGCTGGCGAGGAGGAGCC 300
Qy 591 ACCAAAGACAGCGCGCTGCAGGGGTGTGTGCGCACTTGTGCGAGTGCCTTCCCGCGGG 650
Db 301 ACCAAAGACAGCGCGCTGCAGGGGTGTGTGCGCACTTGTGCGAGTGCCTTCCCGCGGG 360
Qy 651 AACC CGCAACCTTCTTCAGCAGCGCGCTGCGCAACCAAGTCCCAAGCAGCAGCAGCTGAG 710
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Qy 711 GAAGAGCAGTGGCTGCAGTGCAGCTGCGCAAGGCTGAGGCGCATGGCTTTCTTTCGAAGAG 770
Db 421 GAAGAGCAGTGGCTGCAGTGCAGCTGCGCAAGGCTGAGGCGCATGGCTTTCTTTCGAAGAG 480
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Db 1021 ATGAAGGTGGCAAGCCCATCACCCAGAGGCTGGAAACCAATGGTTACATGGCTCCTGAG 1080
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Qy 1431 ATTTATGAATGGTTTGTGGAGCAACCACTTCAAGAGTTCAGAGGAAAGGTTCAGTAAA 1490
Db 1141 ATTTATGAATGGTTTGTGGAGCAACCACTTCAAGAGTTCAGAGGAAAGGTTCAGTAAA 1200
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QY 1491 GAGGATCTGAGCAAGAACTCTGCAAGACGAGGTCAAAATTCAGCATGATACTTCACA 1550
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Db 1201 GAGGATCTGAGCAAGAACTCTGCAAGACGAGGTCAAAATTCAGCATGATACTTCACA 1260
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QY 1551 GAGGAAGCAAAAGATATTTGAGGCTCTCTTGGCTTAAGAAACCGAGCAACGCTTAGGA 1610
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Db 1261 GAGGAAGCAAAAGATATTTGAGGCTCTCTTGGCTTAAGAAACCGAGCAACGCTTAGGA 1320
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QY 1611 AGCAGAGAAAGTCTGATCATCCAGGAAACATCTTTCTTTAAACGATCAACTTCTCT 1670
| | | | |
Db 1321 AGCAGAGAAAGTCTGATCATCCAGGAAACATCTTTCTTTAAACGATCAACTTCTCT 1380
| | | | |
QY 1671 CCGCTGGAAGCTGGCTTAATGAACCCCAATTTGTGCCAGACCTTTCAGTGGTTTATGCC 1730
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Db 1381 CGCCTGGAAGCTGGCTTAATGAACCCCAATTTGTGCCAGACCTTTCAGTGGTTTATGCC 1440
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QY 1731 AAAGACATCGCTGAATGATGATTTCTCTGAGTTTGGGGGTGGAAATTTGATGACAAA 1790
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Db 1441 AAAGACATCGCTGAATGATGATTTCTCTGAGTTTGGGGGTGGAAATTTGATGACAAA 1500
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QY 1791 GATAAGCAGTTCTTCAAAAACCTTTGGACAGGTGCTGTTTCTTATAGCATGGCAGGAAGA 1850
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Db 1501 GATAAGCAGTTCTTCAAAAACCTTTGGACAGGTGCTGTTTCTTATAGCATGGCAGGAAGA 1560
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QY 1851 ATTATAGAAACGGGACTGTTGAGGAACCTGAATGACCCCAACAGACCTACGGGTTGTGAG 1910
| | | | |
Db 1561 ATTATAGAAACGGGACTGTTGAGGAACCTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
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QY 1911 GAGGCTAATTCATCCAGCTCTGGCGTGTGTTGTTTATG 1949
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Db 1621 GAGGCTAATTCATCCAGCTCTGGCGTGTGTTGTTTATG 1659
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RESULT 5

US-10-311-034-45
; Sequence 45, Application US/10311034
; Publication NO. US20040023242A1

; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.

; APPLICANT: YUE, Henry
; APPLICANT: LAL, Preeti

; APPLICANT: BANDMAN, Olga
; APPLICANT: BOROWSKY, Mark L.

; APPLICANT: AU-YOUNG, Janice
; APPLICANT: LU, Yan

; APPLICANT: GANDHI, Ameena R.
; APPLICANT: TRIBOULEY, Catherine M.

; APPLICANT: CHAWLA, Narinder K.
; APPLICANT: YAO, Monique G.

; APPLICANT: LU, Dying Aina M.
; APPLICANT: GREENWALD, Sara R.

; APPLICANT: RAMKUMAR, Jayalaxmi
; APPLICANT: GRIFFIN, Jennifer A.

; APPLICANT: KEARNEY, Liam
; APPLICANT: BURFORD, Neil

; APPLICANT: NGUYEN, Daniel B.
; APPLICANT: TANG, Y. Tom

; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: HE, Ann

; APPLICANT: THORNTON, Michael
; APPLICANT: HAFALIA, April

; APPLICANT: ARVIZU, Chandra S.
; APPLICANT: GURURAJAN, Rajagopal

; APPLICANT: LO, Terence P.
; APPLICANT: KHAH, Farrah A.

; APPLICANT: RECIPON, Shirley A.
; APPLICANT: AZIMZAI, Yalda

; APPLICANT: POLICKY, Jennifer L.
; APPLICANT: DING, Li

; APPLICANT: GRETHER, Megan
; APPLICANT: ELLIOTT, Vicki S.

; APPLICANT: THANGAVELU, Kavitha
; APPLICANT: BATRA, Sajeew

; APPLICANT: ISON, Craig H.
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0125 PCT
; CURRENT APPLICATION NUMBER: US/10/311,034
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372;
60/228,056
; PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-07-25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PERL Program
; SEQ ID NO 45
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040023242A1 7477204CB1
US-10-311-034-45

Query Match 75.5%; Score 1658.8; DB 17; Length 1662;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1660; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 291 ATGTGTGACATGGGGGCCCTGGACAACTGATCGCCAAACACCGCTACCTGCAGGCCCGG 350
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Db 1 ATGTGTGACATGGGGGCCCTGGACAACTGATCGCCAAACACCGCTACCTGCAGGCCCGG 60
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QY 351 AAGCCCTCGACTCGGACAGCAAGAGCTGAGGGGGGGGGGGCTAGCTGGCCCTGCCCC 410
| | | | |
Db 61 AAGCCCTCGACTCGGACAGCAAGAGCTGAGGGGGGGGGGGCTAGCTGGCCCTGCCCC 120
| | | | |
QY 411 GGGCTGACAGGCTCGCGGAGCTCCGCGAGAGCTGCTTGAATCTTCCAGACTTCCACAGCCTGTGT 470
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Db 121 GGGCTGACAGGCTCGCGGAGCTCCGCGAGAGCTGCTTGAATCTTCCAGACTTGTGT 180
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QY 471 GAGCAGCAGCCCATCGGTGCGCGCTCTTCCGTGACTTCTTAGCCACAGTGCACAGTCCACGTTTC 530
| | | | |
Db 181 GAGCAGCAGCCCATCGGTGCGCGCTCTTCCGTGACTTCTTAGCCACAGTGCACAGTTC 240
| | | | |
QY 531 CGCAAGCGGCAACCTTCTTAGAGGAGCTGCGAGAACTGGGAGCTGGCGGAGGAGGACCC 590
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Db 241 CGCAAGCGGCAACCTTCTTAGAGGAGCTGCGAGAACTGGGAGCTGGCGGAGGAGGACCC 300
| | | | |
QY 591 ACCAAAGACAGCGGCTGCGAGGGCTGCTGGCCACTTGTGCGAGTGCCTTCCCGCCCGGG 650
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Db 301 ACCAAAGACAGCGGCTGCGAGGGCTGCTGGCCACTTGTGCGAGTGCCTTCCCGCCCGGG 360
| | | | |
QY 651 AACCCGCAACCTTCTTAGAGGAGCTGCGAGAACTGGGAGCTGGCGGAGGAGGACCC 710
| | | | |
Db 361 AACCCGCAACCTTCTTAGAGGAGCTGCGAGAACTGGGAGCTGGCGGAGGAGGACCC 420
| | | | |
QY 711 GAAGAGCGAGTGGCTGAGTGAAGCTGCGGCAAGCTGAGGCACTGGCTTCTTTCAGAGAG 770
| | | | |
Db 421 GAAGAGCGAGTGGCTGAGTGAAGCTGCGGCAAGCTGAGGCACTGGCTTCTTTCAGAGAG 480
| | | | |
QY 771 CAGCCCTTTAAGGATTTCTGACAGCGCTTCTTACCAAGTCTTCTGAGTGGAACTC 830
| | | | |
Db 481 CAGCCCTTTAAGGATTTCTGACAGCGCTTCTTACCAAGTCTTCTGAGTGGAACTC 540
| | | | |
QY 831 TTGAGATGCAACAGGTGTCAGACAAAGTACTTCACTGAGTTCAGAGTGTGGGAAAGGT 890
| | | | |
Db 541 TTGAGATGCAACAGGTGTCAGACAAAGTACTTCACTGAGTTCAGAGTGTGGGAAAGGT 600
| | | | |
QY 891 GGTTTTGGGAGGTATGTGCGCTCCAGGTGCAAAACACTGGGAGAGTGTATGCTGTAAAG 950
| | | | |
Db 601 GGTTTTGGGAGGTATGTGCGCTCCAGGTGCAAAACACTGGGAGAGTGTATGCTGTAAAG 660
| | | | |
QY 951 AAACCTGACAAAGAGCGGCTGAAGAGAGAAAGGTGGCGAGAGAGTGGCTCTCTTGGAAAG 1010
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Db 661 AAACCTGACAAAGAGCGGCTGAAGAGAGAAAGGTGGCGAGAGAGTGGCTCTCTTGGAAAG 720
| | | | |
QY 1011 GAAATCTTGAGAAAGGTTCAGACGCCCTTTTCATTTGTCTCTCTGGCCTATGCTTTGAGAGC 1070
| | | | |

Db 721 GAAATCTTGGGAAGGTGAGAGCCTTTCATGTCTCTGGCCTATGCTTTCAGAGC 780
Qy 1071 AAGACCCATCTCTGCTTGTATGAGCCTGATGAATGGGGAGAGCCTCAAGTTTCACATC 1130
Db 781 AAGACCCATCTCTGCTTGTATGAGCCTGATGAATGGGGAGAGCCTCAAGTTTCACATC 840
Qy 1131 TACAACGTGGGACGCGTGGCTGAGCATGAGCAGCGGTGATCTTTTACTCGGCCAGATA 1190
Db 841 TACAACGTGGGACGCGTGGCTGAGCATGAGCAGCGGTGATCTTTTACTCGGCCAGATA 900
Qy 1191 GCCTGTGGATGCTGACCTCCATCAACTCGGCATCGTCTATCGGACATGAAGCCTGAG 1250
Db 901 GCCTGTGGATGCTGACCTCCATCAACTCGGCATCGTCTATCGGACATGAAGCCTGAG 960
Qy 1251 AATGTGCTTCTGGATGACCTCGCAACTGCGAGTTTATCTGACCTGGGGCTGGCCGTGGAG 1310
Db 961 AATGTGCTTCTGGATGACCTCGCAACTGCGAGTTTATCTGACCTGGGGCTGGCCGTGGAG 1020
Qy 1311 ATGAAGGTGGCAAGCCATCAACCAGAGGGCTGGAACCAATGGTTACATGGCTCTGAG 1370
Db 1021 ATGAAGGTGGCAAGCCATCAACCAGAGGGCTGGAACCAATGGTTACATGGCTCTGAG 1080
Qy 1371 ATCTTAATGGAAGGTAAAGTTATCTCTATCTGTGGACTGTTTGGCCATGGGATGAGC 1430
Db 1081 ATCTTAATGGAAGGTAAAGTTATCTCTATCTGTGGACTGTTTGGCCATGGGATGAGC 1140
Qy 1431 ATTTATGAATGTTGCTGGAGCAACACCATTTCAAGATTAACAAGAAAGGTCAAGTAA 1490
Db 1141 ATTTATGAATGTTGCTGGAGCAACACCATTTCAAGATTAACAAGAAAGGTCAAGTAA 1200
Qy 1491 GAGGATCTGAAGCAAGAACTCTGCAAGACGAGGTCAAAATTCAGCATGATACTTACA 1550
Db 1201 GAGGATCTGAAGCAAGAACTCTGCAAGACGAGGTCAAAATTCAGCATGATACTTACA 1260
Qy 1551 GAGGAAGCAAAAGATATTGCAAGCTCTTCTGGCTAAGAAACAGAGCAAGCTTAGGA 1610
Db 1261 GAGGAAGCAAAAGATATTGCAAGCTCTTCTGGCTAAGAAACAGAGCAAGCTTAGGA 1320
Qy 1611 AGCAGAGAAAGTCTGATGATCCAGGAAACATCATTTCTTTAAACGATCAACTTCT 1670
Db 1321 AGCAGAGAAAGTCTGATGATCCAGGAAACATCATTTCTTTAAACGATCAACTTCT 1380
Qy 1671 GCCTGGAAGCTGGCTAATTAAGACCCCATTTGTGCCAGACCTTCAGTGGTTATGCC 1730
Db 1381 GCCTGGAAGCTGGCTAATTAAGACCCCATTTGTGCCAGACCTTCAGTGGTTATGCC 1440
Qy 1731 AAAGCATCGCTGAATGATGATTTCTGAGGTTGGGGGGTGGAAATTTGATGACAAA 1790
Db 1441 AAAGCATCGCTGAATGATGATTTCTGAGGTTGGGGGGTGGAAATTTGATGACAAA 1500
Qy 1791 GATAGCAGTTCTTCAAAACCTTTCGACAGCTGCTGTTCTATAGCATGGCAGGAAGA 1850
Db 1501 GATAGCAGTTCTTCAAAACCTTTCGACAGCTGCTGTTCTATAGCATGGCAGGAAGA 1560
Qy 1851 ATTATAGAAACGGGACTGTTTGGAGAACTGAATGACCCCAACAGACCTACGGGTTGAG 1910
Db 1561 ATTATAGAAACGGGACTGTTTGGAGAACTGAATGACCCCAACAGACCTACGGGTTGAG 1620
Qy 1911 GAGGTAATTCATCAAGTCTGGCGTGTGTTGTTTATTGTAA 1952
Db 1621 GAGGTAATTCATCAAGTCTGGCGTGTGTTGTTTATTGTAA 1662

RESULT 6

US-10-451-168-49
; Sequence 49, Application US/10451168
; Publication No. US20040091969A1
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM P.L.C.
; APPLICANT: GLAXO GROUP LIMITED
; TITLE OF INVENTION: NOVEL COMPOUNDS

; FILE REFERENCE: GP50039
; CURRENT APPLICATION NUMBER: US/10/451,168
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/US01/49232
; PRIOR FILING DATE: 2000-12-17
; PRIOR APPLICATION NUMBER: 60/256,710
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/257,048
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/260,482
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/264,922
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/266,797
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/276,988
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/281,535
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/289,622
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-451-168-49

Query Match 75.5%; Score 1658.8; DB 17; Length 1662;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1660; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 291 ATGTGGACATGGGGGCGCTCGACAACTGATCGCAACACCGCTACTGTGAGCCCGG 350
Db 1 ATGTGGACATGGGGGCGCTCGACAACTGATCGCAACACCGCTACTGTGAGCCCGG 60
Qy 351 AAGCCCTCGACTGCGACAGCAAAAGAGCTGAGCGGGCGGGCTAGCTGCGCCCTGCC 410
Db 61 AAGCCCTCGACTGCGACAGCAAAAGAGCTGAGCGGGCGGGCTAGCTGCGCCCTGCC 120
Qy 411 GGGCTGAGGGCTCGGGGAGCTCGCGAGAGCTGCTCCCTGACCTTCCACAGCCCTGT 470
Db 121 GGGCTGAGGGCTCGGGGAGCTCGCGAGAGCTGCTCCCTGACCTTCCACAGCCCTGT 180
Qy 471 GAGCAGAGCCCATCGGTGCGCGCTCTTCCGTGACTTCTAGCCACAGTGCACAGTTTC 530
Db 181 GAGCAGAGCCCATCGGTGCGCGCTCTTCCGTGACTTCTAGCCACAGTGCACAGTTTC 240
Qy 531 CGCAAGCGCGCAACTTCTTAGAGGACGTGAGAACTGGGAGCTGGCGAGGAGGAGCCC 590
Db 241 CGCAAGCGCGCAACTTCTTAGAGGACGTGAGAACTGGGAGCTGGCGAGGAGGAGCCC 300
Qy 591 ACCAAGAGCAGCGCTGCGAGGGCTGCTGGCCACTTGTGCGAGTGCCTTGCCTGCGGGG 650
Db 301 ACCAAGAGCAGCGCTGCGAGGGCTGCTGGCCACTTGTGCGAGTGCCTTGCCTGCGGGG 360
Qy 651 AACCGCAACCTTCTCCTCAGCAGCGCTGCGCCACCAAGTGCAGAGCAGCCACCTGAG 710
Db 361 AACCGCAACCTTCTCCTCAGCAGCGCTGCGCCACCAAGTGCAGAGCAGCCACCTGAG 420
Qy 711 GAAGAGCGAGTGGCTGAGTGAACGTGCGCAAGGCTGAGGGCAATGGCTTTCTTGAAGAG 770
Db 421 GAAGAGCGAGTGGCTGAGTGAACGTGCGCAAGGCTGAGGGCAATGGCTTTCTTGAAGAG 480
Qy 771 CAGCCCTTAAAGGATTTCTGATCCAGCCCTTCTACGCAAGTTTCTGAGTGGGAACTC 830
Db 481 CAGCCCTTAAAGGATTTCTGATCCAGCCCTTCTACGCAAGTTTCTGAGTGGGAACTC 540
Qy 831 TTCGAGATGCAACCAAGTGTGAGAACTTCTACTGAGTTTCTGAGTGTCTGGGAAAGGT 890
Db 541 TTCGAGATGCAACCAAGTGTGAGAACTTCTACTGAGTTTCTGAGTGTCTGGGAAAGGT 600

Qy	951	AAACTGGACAAGAACGGCGCTGAAGAGAAAGGTGGCAGAAAGATGGCTCTCTTTGGAAAAAG	1010
Db	661	AAACTGGACAAGAACGGCGCTGAAGAGAAAGGTGGCAGAAAGATGGCTCTCTTTGGAAAAAG	720
Qy	1011	GAAATCTTTGGAGAAGGTTCAGCAGACCCCTTTCAATTGTCTCTCTGGCCCTATGCTTTTGAGAGC	1070
Db	721	GAAATCTTTGGAGAAGGTTCAGCAGACCCCTTTCAATTGTCTCTCTGGCCCTATGCTTTTGAGAGC	780
Qy	1071	AAGACCCATCTCTGCTCTTGTTCATGAGCGCTGATGAATGGGGGAGACCTCAAGTTTCCACATC	1130
Db	781	AAGACCCATCTCTGCTCTTGTTCATGAGCGCTGATGAATGGGGGAGACCTCAAGTTTCCACATC	840
Qy	1131	TACAACTGGGCAACGCTGGCGCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCCAGATA	1190
Db	841	TACAACTGGGCAACGCTGGCGCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCCAGATA	900
Qy	1191	GCCTGTGGGATGCTGCACCTCCATGAACCTCGGCATCGTCTATCGGGACATGAAGACCTGAG	1250
Db	901	GCCTGTGGGATGCTGCACCTCCATGAACCTCGGCATCGTCTATCGGGACATGAAGACCTGAG	960
Qy	1251	AATGTGCTTTGGAATGACCTCGGCAACTGCGAGTTTATCTGACCTTGGGGCTGGCCGTGGAG	1310
Db	961	AATGTGCTTTGGAATGACCTCGGCAACTGCGAGTTTATCTGACCTTGGGGCTGGCCGTGGAG	1020
Qy	1311	ATGAAGGGTGGCAGACCCATCACCCAGAGGGCTGGACCAATGGTTACATGGCTCCTGAG	1370
Db	1021	ATGAAGGGTGGCAGACCCATCACCCAGAGGGCTGGACCAATGGTTACATGGCTCCTGAG	1080
Qy	1371	ATCCTAATGAAAAGGTAAAGTTATTCCTATCTCTGTGACCTGGTTTGGCATGGGATGCAGC	1430
Db	1081	ATCCTAATGAAAAGGTAAAGTTATTCCTATCTCTGTGACCTGGTTTGGCATGGGATGCAGC	1140
Qy	1431	ATTTATGAAATGGTTGCTGGACGAACACCAATTCAAAGATTTCAAGGAAAAAGTTCAGTAAA	1490
Db	1141	ATTTATGAAATGGTTGCTGGACGAACACCAATTCAAAGATTTCAAGGAAAAAGTTCAGTAAA	1200
Qy	1491	GAGGATCTGAAGCAAAAGAACTCTGTCAAGACGAGGTCAAAATCCAGCATGATACTTCCACA	1550
Db	1201	GAGGATCTGAAGCAAAAGAACTCTGTCAAGACGAGGTCAAAATCCAGCATGATACTTCCACA	1260
Qy	1551	GAGGAAGCAAAAGATAATTTGCGAGGCTCTCTTGGCTAAGAAAAACAGACGAACCTTAGGA	1610
Db	1261	GAGGAAGCAAAAGATAATTTGCGAGGCTCTCTTGGCTAAGAAAAACAGACGAACCTTAGGA	1320
Qy	1611	AGCAGAGAAAAGTCTGATGATCCCAGAGAAACATCATTTTCTTTAAACGATCAACTTTCCT	1670
Db	1321	AGCAGAGAAAAGTCTGATGATCCCAGAGAAACATCATTTTCTTTAAACGATCAACTTTCCT	1380
Qy	1671	CGCCTGGAAGCTGGCCCTAAATTGAACCCCAATTTGTGCGAGACCTTCAGTGGTTTATGCC	1730
Db	1381	CGCCTGGAAGCTGGCCCTAAATTGAACCCCAATTTGTGCGAGACCTTCAGTGGTTTATGCC	1440
Qy	1731	AAAGACATCGCTGAAATTTGATGATTTCTCTGAGGTTCCGGGGGTGGAAATTTGATGACAAA	1790
Db	1441	AAAGACATCGCTGAAATTTGATGATTTCTCTGAGGTTCCGGGGGTGGAAATTTGATGACAAA	1500
Qy	1791	GATGAAGCAGTTCTTCAAAAATTTTGGCAGAGGTGCTGCTTCTATAGCATCGCAGGAGAA	1850
Db	1501	GATGAAGCAGTTCTTCAAAAATTTTGGCAGAGGTGCTGCTTCTATAGCATCGCAGGAGAA	1560
Qy	1851	ATTATAGAAAACGGGACTGTTTGGAGAACTGAAATGACCCCAACAGACCTACGGGTTGTGAG	1910
Db	1561	ATTATAGAAAACGGGACTGTTTGGAGAACTGAAATGACCCCAACAGACCTACGGGTTGTGAG	1620
Qy	1911	GAGGGTAATTCATCCAAAGCTGGCGGTGTTTGTATTGTAA	1952
Db	1621	GAGGGTAATTCATCCAAAGCTGGCGGTGTTTGTATTGTAA	1662

RESULT 8

RESULTS 8
US-09-802-117-1

US-09-802-II/-I
; Sequence 1, Application US/09802117

; sequence 1, Application US/0980.
; Publication No. US20020042503A1

721 GAAATCTTGAGAGAGTCTAGACCCCTTTCAATGTCTCTCTGCGCTATGCTTTGAGAGC 780
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1071 AAGACCCATCTCTGCTTGTCTATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 1130
Qy
781 AAGACCCATCTCTGCTTGTCTATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840
Db
1131 TACAAGCTGGGCAAGCGCTGGCTGGACATGAGCCGGGTGATCTTTTACTCGGCCAGATA 1190
Qy
841 TACAAGCTGGGCAAGCGCTGGCTGGACATGAGCCGGGTGATCTTTTACTCGGCCAGATA 900
Db
1191 GCTGTGGATGCTGACCTCCATGAACTCGCATCTGCTATCGGACATGAGCCTGAG 1250
Qy
901 GCTGTGGATGCTGACCTCCATGAACTCGCATCTGCTATCGGACATGAGCCTGAG 960
Db
1251 AATGTGCTTCTGATGACCTCGGCAATCGACCTTATCTGACCTGGGCTGGCTGGAG 1310
Qy
961 AATGTGCTTCTGATGACCTCGGCAATCGACCTTATCTGACCTGGGCTGGCTGGAG 1020
Db
1311 ATGAAGGTGGCAAGCCCATACCCAGAGGGCTGGAACCAATGGTTACATGGCTCTCTGAG 1370
Qy
1021 ATGAAGGTGGCAAGCCCATACCCAGAGGGCTGGAACCAATGGTTACATGGCTCTCTGAG 1080
Db
1371 ATCTTAATGGAAAGGTAAATTTCTTATCTGCTGGAAGTCTGCTGGAAGTCTGAGC 1430
Qy
1081 ATCTTAATGGAAAGGTAAATTTCTTATCTGCTGGAAGTCTGCTGGAAGTCTGAGC 1140
Db
1431 ATTTATGAAATGGTTGCTGGAGCAACACCAATCAAGATTAACAAGAAAGGTCAATAA 1490
Qy
1141 ATTTATGAAATGGTTGCTGGAGCAACCAATCAAGATTAACAAGAAAGGTCAATAA 1200
Db
1491 GAGGATCTGAAGCAAGAACTCTGCAAGAGGTCAAATTCAGCATGATACTTTACA 1550
Qy
1201 GAGGATCTGAAGCAAGAACTCTGCAAGAGGTCAAATTCAGCATGATACTTTACA 1260
Db
1551 GAGGAGCAAGAAATTTGAGGCTCTTCTGCTGAGAAACATCAATTTCTTAAACGATCAACTTTCT 1610
Qy
1261 GAGGAGCAAGAAATTTGAGGCTCTTCTGCTGAGAAACATCAATTTCTTAAACGATCAACTTTCT 1320
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1321 AGCAGAGAAAGTCTGATGATCCAGGAAACATCAATTTCTTAAACGATCAACTTTCT 1380
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Qy
1381 GCGCTGGAAGCTGGCTTAATGAACCCCATTTGTGCGAGACCCCTTCAAGTGGTTATGCC 1440
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Qy
1441 AAGAGCATCGCTGAAATTTGATGATTTCTGAGGTTGCGGGGTGGAAATTTGATGACAAA 1500
Db
1791 GATAAGCAGTTCTTCAAAAACCTTTGCGACAGGTGCTGTTCTTATAGCATGGCAGGAAGAA 1850
Qy
1501 GATAAGCAGTTCTTCAAAAACCTTTGCGACAGGTGCTGTTCTTATAGCATGGCAGGAAGAA 1560
Db
1851 ATTAAGAAACGGGACTGTTGAGAACTGAATGACCCCAACAGACCTTACGGTTGAG 1910
Qy
1561 ATTAAGAAACGGGACTGTTGAGAACTGAATGACCCCAACAGACCTTACGGTTGAG 1620
Db
1911 GAGGTAATTCATCAAGCTGGGCTGTTGTTGTTATGTA 1952
Qy
1621 GAGGTAATTCATCAAGCTGGGCTGTTGTTGTTATGTA 1662
Db

RESULT 9

US-10-217-745-1
; Sequence 1, Application US/10217745
; Publication No. US20030004328A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. US20030004328A1el Human G-Coupled Protein Receptor Kinases an
; TITLE OF INVENTION: Polynucleotides

; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/10/217,745
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US/09/802,117
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: homo sapiens
; US-10-217-745-1

Query Match 75.5%; Score 1658.4; DB 14; Length 1662;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1659; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 291 ATGTGGACATGGGGGCGCTTGGCAACCTGATGCCCAACACCGCTTACCTGCGAGCCCGG 350
Db 1 ATGTGGACATGGGGGCGCTTGGCAACCTGATGCCCAACACCGCTTACCTGCGAGCCCGG 60
Qy 351 AAGCCCTCGACTCGGACAGCAAGAGCTGAGCGCGCGGCTAGCTGGCCCTGCC 410
Db 61 AAGCCCTCGACTCGGACAGCAAGAGCTGAGCGCGCGGCTAGCTGGCCCTGCC 120
Qy 411 GGGCTGAGGGCTGCGCGGAGCTCCGCGAGAGCTCCGCGAGAGCTGCTTCCAGCTTCC 470
Db 121 GGGCTGAGGGCTGCGCGGAGCTCCGCGAGAGCTGCTTCCAGCTTCCAGCTTCC 180
Qy 471 GAGCAGAGCCCATCGGTGCGCGCTTCTTCCGTGACTTCTTAGCCACAGTGCCACCTTC 530
Db 181 GAGCAGAGCCCATCGGTGCGCGCTTCTTCCGTGACTTCTTAGCCACAGTGCCACCTTC 240
Qy 531 GCGAGCGCGCAACCTTCTTAGAGAGCTGCGAGAACTGGAGAGTGGCCGAGAGAGCC 590
Db 241 GCGAGCGCGCAACCTTCTTAGAGAGCTGCGAGAACTGGAGAGTGGCCGAGAGAGCC 300
Qy 591 ACCAAGACAGCGCTGCAAGGGCTGCTGCGCACTTGTGCGAGTGGCCCTGCCCGGG 650
Db 301 ACCAAGACAGCGCTGCAAGGGCTGCTGCGCACTTGTGCGAGTGGCCCTGCCCGGG 360
Qy 651 AACCCGCAACCTTCTTAGCCAGCGCTGCGCAACCAAGTGCAGAGCAGCACCCTGAG 710
Db 361 AACCCGCAACCTTCTTAGCCAGCGCTGCGCAACCAAGTGCAGAGCAGCACCCTGAG 420
Qy 711 GAAGAGGAGTGGCTGAGTGGCTGCGCAACCAAGTGCAGAGCAGCACCCTGAG 770
Db 421 GAAGAGGAGTGGCTGAGTGGCTGCGCAACCAAGTGCAGAGCAGCACCCTGAG 480
Qy 771 CAGCCCTTAAAGATTTGCTGACAGCGCTTCTAGCAAGTTTCTGCAAGTGGAACTC 830
Db 481 CAGCCCTTAAAGATTTGCTGACAGCGCTTCTAGCAAGTTTCTGCAAGTGGAACTC 540
Qy 831 TTCAGATGCAACAGGTGTCAGAAAGTACTTCACTGAGTTTCAAGTGGGGAAGGT 890
Db 541 TTCAGATGCAACAGGTGTCAGAAAGTACTTCACTGAGTTTCAAGTGGGGAAGGT 600
Qy 891 GGTGTTGGGAGGTATGTCGCTTCCAGTGAAGAAACACTGGGAAGATGATGCTGTAAG 950
Db 601 GGTGTTGGGAGGTATGTCGCTTCCAGTGAAGAAACACTGGGAAGATGATGCTGTAAG 660
Qy 951 AAATGGCAAGAGCGGCTGAAGAAAGAGTGGCGAGAGATGGCTCTCTTGGAAAG 1010
Db 661 AAATGGCAAGAGCGGCTGAAGAAAGAGTGGCGAGAGATGGCTCTCTTGGAAAG 720
Qy 1011 GAAATCTTGAGAGGTGAGAGCCCTTTCATTTGTTCTTCTGCGCTTATGCTTTGAGC 1070
Db 721 GAAATCTTGAGAGGTGAGAGCCCTTTCATTTGTTCTTCTGCGCTTATGCTTTGAGC 780
Qy 1071 AAGACCCATCTCTGCTTGTGATGAGCCCTGATGAATGGGGGAGACCTCAAGTCCACATC 1130
Db 781 AAGACCCATCTCTGCTTGTGATGAGCCCTGATGAATGGGGGAGACCTCAAGTCCACATC 840


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QY 1131 TACAACGTGGGACGCGTGGCTGGACATGAGCCGGTGATCTTTTACTCGGCCAGATA 1190
Db 841 TACAACGTGGGACGCGTGGCTGGACATGAGCCGGTGATCTTTTACTCGGCCAGATA 900
QY 1191 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATGCTTATCGGCACATGAAGCTGAG 1250
Db 901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATGCTTATCGGCACATGAAGCTGAG 960
QY 1251 AATGTGCTTCTGGATGACCTCGGCAACTCGAGCTTATCTGACTGGGGCTGGCCGTGGAG 1310
Db 961 AATGTGCTTCTGGATGACCTCGGCAACTCGAGCTTATCTGACTGGGGCTGGCCGTGGAG 1020
QY 1311 ATGAAGGGTGGCAAGCCCATCAACCCAGAGGGCTGGAACCAATGGTTATCATGCTCTGAG 1370
Db 1021 ATGAAGGGTGGCAAGCCCATCAACCCAGAGGGCTGGAACCAATGGTTATCATGCTCTGAG 1080
QY 1371 ATCCCTAATGGAAAGGTAGTTATTTCCTATCTGTGGACTGTTTCCCATGGGATGCAGC 1430
Db 1081 ATCCCTAATGGAAAGGTAGTTATTTCCTATCTGTGGACTGTTTCCCATGGGATGCAGC 1140
QY 1431 ATTTATGAAATGGTGTGGACGAACACCACTTCAAGATTACAAGGAAAGGTCAAGTAA 1490
Db 1141 ATTTATGAAATGGTGTGGACGAACACCACTTCAAGATTACAAGGAAAGGTCAAGTAA 1200
QY 1491 GAGGATCTGAAGCAAGAACTCTGCAAGACGAGGTCAAATTCAGCATGATAACTTCA 1550
Db 1201 GAGGATCTGAAGCAAGAACTCTGCAAGACGAGGTCAAATTCAGCATGATAACTTCA 1260
QY 1551 GAGGAAGCAAGATATTTCGAGGCTTCTTGGCTTAAGAACCCAGGACGCTTAGGA 1610
Db 1261 GAGGAAGCAAGATATTTCGAGGCTTCTTGGCTTAAGAACCCAGGACGCTTAGGA 1320
QY 1611 AGCAGAGAAAGCTGTGATGATCCAGGAAACATCTTTCTTTAAACAGTCAACTTCT 1670
Db 1321 AGCAGAGAAAGCTGTGATGATCCAGGAAACATCTTTCTTTAAACAGTCAACTTCT 1380
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Db 1561 ATTATAGAAACGGGACTGTTTGAGGAACCTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
QY 1911 GAGGATAATTCATCAAGTCTGGGCTGGTGGTTGTTGTTATGTAA 1952
Db 1621 GAGGATAATTCATCAAGTCTGGGCTGGTGGTTGTTGTTATGTAA 1662
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RESULT 10

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US-09-964-469-1
; Sequence 1, Application US/09964469
; Patent No. US20020034803A1
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000636DIV
; CURRENT APPLICATION NUMBER: US/09/964,469
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 60/208,331
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: 09/738,894
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; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Human
; US-09-964-469-1

Query Match      75.4%; Score 1657.2; DB 9; Length 1662;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1659; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 291 ATGTGTGAGATGCGGGGCCCTGGACAACTGTGACCAACCTGATCGCAACCTGATCGCAACCTGATCGAGGCCCG 350
Db 1 ATGTGTGAGATGCGGGGCCCTGGACAACTGTGACCAACCTGATCGCAACCTGATCGAGGCCCG 60

QY 351 AAGCCCTCGGACTGCGACAGCAAGAGCTGCAGCGCGCGCGGTAGCTTGGCCCTGCCCC 410
Db 61 AAGCCCTCGGACTGCGACAGCAAGAGCTGCAGCGCGCGCGGTAGCTTGGCCCTGCCCC 120

QY 411 GGGCTGCAAGGGCTGCGCGAGCTCGCGCAGAAAGTGTCCCTGAACTTCCACAGCCTGTGT 470
Db 121 GGGCTGCAAGGGCTGCGCGAGCTCGCGCAGAAAGTGTCCCTGAACTTCCACAGCCTGTGT 180

QY 471 GAGCAGCAGCCCATCGTTCGCCGCCCTCTTCGGTGAATTCCTAGCCACAGTGCCTCAGTTTC 530
Db 181 GAGCAGCAGCCCATCGTTCGCCGCCCTCTTCGGTGAATTCCTAGCCACAGTGCCTCAGTTTC 240

QY 531 CGAAGGCGGCAACCTTCCTAGAGAGAGCTGCAGAACTGGGAGCTGGCGAGGAGGACCC 590
Db 241 CGAAGGCGGCAACCTTCCTAGAGAGAGCTGCAGAACTGGGAGCTGGCGAGGAGGACCC 300

QY 591 ACCAAGACAGCGCGCTCGAGGGGCTGTGGCCACTTGTGCGAGTGCCTTCGCCCGGG 650
Db 301 ACCAAGACAGCGCGCTCGAGGGGCTGTGGCCACTTGTGCGAGTGCCTTCGCCCGGG 360

QY 651 AACCGCAACCTTCCTCAGCCAGCGCGTGGCCACCAAGTGCACAGCAGCCCACTGAG 710
Db 361 AACCGCAACCTTCCTCAGCCAGCGCGTGGCCACCAAGTGCACAGCAGCCCACTGAG 420

QY 711 GAAGAGCAGTGGCTGAGTGAAGCTGCAGAAAGCTGAGGCCATGGCTTCTTTCGAGAG 770
Db 421 GAAGAGCAGTGGCTGAGTGAAGCTGCAGAAAGCTGAGGCCATGGCTTCTTTCGAGAG 480

QY 771 CAGCCCTTTAAGGATTTCTGACAGCAGCGCTTCTACGACAAGTTCCTGAGTGGAAATCTC 830
Db 481 CAGCCCTTTAAGGATTTCTGACAGCAGCGCTTCTACGACAAGTTCCTGAGTGGAAATCTC 540

QY 831 TTGAGATGCAACCAAGTGTCAAGCAAGTACTTCACTGAGTTCAGAGTGTGCGGGAAGGT 890
Db 541 TTGAGATGCAACCAAGTGTCAAGCAAGTACTTCACTGAGTTCAGAGTGTGCGGGAAGGT 600

QY 891 GGTTTTGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAAGATGATATGCTGTAA 950
Db 601 GGTTTTGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAAGATGATATGCTGTAA 660

QY 951 AAACCTGGACAGAGCGGCTGAAGAAAGAGTGGCGAGAGATGGCTTCTTTCGAAAG 1010
Db 661 AAACCTGGACAGAGCGGCTGAAGAAAGAGTGGCGAGAGATGGCTTCTTTCGAAAG 720

QY 1011 GAAATCTTGGAGAGGTGAGCAGCGCTTTCATTTGTTCTCTGCGCTATGCTTTCAGAGC 1070
Db 721 GAAATCTTGGAGAGGTGAGCAGCGCTTTCATTTGTTCTCTGCGCTATGCTTTCAGAGC 780

QY 1071 AAGACCCATCTCTGCTTGTGATGAGCTGATGAATGGGGAGAGCCTCAAGTTCACATC 1130
Db 781 AAGACCCATCTCTGCTTGTGATGAGCTGATGAATGGGGAGAGCCTCAAGTTCACATC 840

QY 1131 TACAACGTGGGACGCGTGGCTGACATGAGCGGGTGATCTTTTACTCGGCCAGATA 1190
Db 841 TACAACGTGGGACGCGTGGCTGACATGAGCGGGTGATCTTTTACTCGGCCAGATA 900
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1191 GCCTGTGGGATGCTGCACCTCCATGAACCTCGCATCGTCTATCGGACATGAAGCTGAG 1250
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901  GCCTGTGGGATGCTGCACCTCCATGAACCTCGCATCGTCTATCGGACATGAAGCTGAG 960
QY      |||
1251 AATGTGCTTCTGATGACCTCGGCAACTGCGGCTTATCTGACCTGGGGCTGGCCGTGGAG 1310
Db      |||
961  AATGTGCTTCTGATGACCTCGGCAACTGCGGCTTATCTGACCTGGGGCTGGCCGTGGAG 1020
QY      |||
1311 ATGAAGGGTGGCAAGCCCATCACCCAGAGGCTGGAAACCAATGTTACATGGCTCTGAG 1370
Db      |||
1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGCTGGAAACCAATGTTACATGGCTCTGAG 1080
QY      |||
1371 ATCTTAATGAAAGAGTAACTTATCTATCTCTGTGGAAGTGGTTTCCATGGGATGACG 1430
Db      |||
1081 ATCTTAATGAAAGAGTAACTTATCTATCTCTGTGGAAGTGGTTTCCATGGGATGACG 1140
QY      |||
1431 ATTATGAAATGTTGCTGGAAGCAACCAATTCAGAAATTAACAAGAAAGTTCAGTAAA 1490
Db      |||
1141 ATTATGAAATGTTGCTGGAAGCAACCAATTCAGAAATTAACAAGAAAGTTCAGTAAA 1200
QY      |||
1491 GAGGATCTGAAGCAAGAACTCTGCAAGACGAGGTCAAAATTCAGCATGATTAACCTTACA 1550
Db      |||
1201 GAGGATCTGAAGCAAGAACTCTGCAAGACGAGGTCAAAATTCAGCATGATTAACCTTACA 1260
QY      |||
1551 GAGGAAGCAAGAAATTTGCAAGCTCTTTCTGGCTAAGAAACAGAGCAACGCTTAGGA 1610
Db      |||
1261 GAGGAAGCAAGAAATTTGCAAGCTCTTTCTGGCTAAGAAACAGAGCAACGCTTAGGA 1320
QY      |||
1611 AGCAGAGAAAGTCTGATGATCCAGGAAACATCATTTCTTTAAACGATCAACTTCTCT 1670
Db      |||
1321 AGCAGAGAAAGTCTGATGATCCAGGAAACATCATTTCTTTAAACGATCAACTTCTCT 1380
QY      |||
1671 CGCTCGAAGCTGGCCCTAATTTGAACCCCATTTGTGCCAGACCTTCACTGGTGTATGCC 1730
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QY      |||
1731 AAGACATCGCTGAAATGATGATTTCTCTGAGGTTTCGGGGGTGGAATTTGATGACAAA 1790
Db      |||
1441 AAGACATCGCTGAAATGATGATTTCTCTGAGGTTTCGGGGGTGGAATTTGATGACAAA 1500
QY      |||
1791 GATAGCAGTCTTCAAAACCTTTGGCAGAGTGTCTTCTATAGCATGGCAGGAAGA 1850
Db      |||
1501 GATAAGCAGTCTTCAAAACCTTTGGCAGAGTGTCTTCTATAGCATGGCAGGAAGA 1560
QY      |||
1851 ATTATAGAAACGGGACTGTTTGAGGAACCTGAATGACCCCAACAGACCTACGSGTTGTGAG 1910
Db      |||
1561 ATTATAGAAACGGGACTGTTTGAGGAACCTGAATGACCCCAACAGACCTACGSGTTGTGAG 1620
QY      |||
1911 GAGGTAATTCATCCAAAGTCTCGGCTGTGTTGTTTATTGTAA 1952
Db      |||
1621 GAGGTAATTCATCCAAAGTCTCGGCTGTGTTGTTTATTGTAA 1662
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RESULT 11

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US-10-425-962-1
; Sequence 1, Application US/10425962
; Publication No. US20030180786A1
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000636DIV2
; CURRENT APPLICATION NUMBER: US/10/425,962
; PRIORITY FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 09/964,469
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 09/738,894
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/208,331
; PRIOR FILING DATE: 2000-06-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 1
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-425-962-1
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Query Match
Best Local Similarity 75.4%; Score 1657.2; DB 16; Length 1662;
Matches 1659; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 291 ATGTGTGACATGGGGGCGCTCGACAACTGATCGCAACACGCTACTCGCAGCCCGG 350
Db      |||
1  ATGTGTGACATGGGGGCGCTCGACAACTGATCGCAACACGCTACTCGCAGCCCGG 60
QY 351 AAGCCTCTCGAATGCGACAGCAAAAGAGCTGAGGGGGCGGCGGTAGCCTTGCCCTGCC 410
Db      |||
61  AAGCCTCTCGAATGCGACAGCAAAAGAGCTGAGGGGGCGGCGGTAGCCTTGCCCTGCC 120
QY 411 GGGCTGCAAGGCTGGGGGCGCTCGCAGAAAGCTGTCCTGAACTTCCACAGCCTGTGT 470
Db      |||
121 GGGCTGCAAGGCTGGGGGCGCTCGCAGAAAGCTGTCCTGAACTTCCACAGCCTGTGT 180
QY 471 GAGCAGCAGCCCATCGGCTCGCGGCTCTTTCGCTGACTTCTTAGCCACAGTGCACACGTTTC 530
Db      |||
181 GAGCAGCAGCCCATCGGCTCGCGGCTCTTTCGCTGACTTCTTAGCCACAGTGCACACGTTTC 240
QY 531 CGCAAGGGCGCAACTTCTTAGAGAGCTGTCAGAACTGGGGAGCTGGCCGAGAGGAGCC 590
Db      |||
241 CGCAAGGGCGCAACTTCTTAGAGAGCTGTCAGAACTGGGGAGCTGGCCGAGAGGAGCC 300
QY 591 ACCAAAGACAGCGGCTGCGAGGGCTGTCGCCACTTGTGCGAGTGCCTGCCCGCGGG 650
Db      |||
301 ACCAAAGACAGCGGCTGCGAGGGCTGTCGCCACTTGTGCGAGTGCCTGCCCGCGGG 360
QY 651 AACCCGCAACCTTCTCTCAGCAGCGGCTGCGCAACCAAGTGCACAGCAGCCACCTGAG 710
Db      |||
361 AACCCGCAACCTTCTCTCAGCAGCGGCTGCGCAACCAAGTGCACAGCAGCCACCTGAG 420
QY 711 GAAAGAGAGTGGCTGAGTGAAGCTGCGGAGGCTGAGGCCATGGCTTCTTGCAGAGAG 770
Db      |||
421 GAAAGAGAGTGGCTGAGTGAAGCTGCGGAGGCTGAGGCCATGGCTTCTTGCAGAGAG 480
QY 771 CAGCCCTTTAAGGATTTCTGACAGCGCTTCTTACGACAAAGTTTCTGCGAGTGAAGCTC 830
Db      |||
481 CAGCCCTTTAAGGATTTCTGACAGCGCTTCTTACGACAAAGTTTCTGCGAGTGAAGCTC 540
QY 831 TTCAGATGCAACAGTGTGAGCAAGTACTTCACTCAGTTCAGAGTGTCTGGGAAAGGT 890
Db      |||
541 TTCAGATGCAACAGTGTGAGCAAGTACTTCACTCAGTTCAGAGTGTCTGGGAAAGGT 600
QY 891 GGTTCGGGAGGTATGTCGCTCCAGGTGCAAAACACTGGGAGAGTATGCTGTGAG 950
Db      |||
601 GGTTCGGGAGGTATGTCGCTCCAGGTGCAAAACACTGGGAGAGTATGCTGTGAG 660
QY 951 AAACCTGCAAGAGCGGCTGCAAGAGAGTGGCGAGAGAGTGGCTCTCTTGGAAAAAG 1010
Db      |||
661 AAACCTGCAAGAGCGGCTGCAAGAGAGTGGCGAGAGAGTGGCTCTCTTGGAAAAAG 720
QY 1011 GAAATCTTGGAGAGGTGAGCAGCCCTTTTCATGCTCTCTGCGCTTATGCTTTGAGAGC 1070
Db      |||
721 GAAATCTTGGAGAGGTGAGCAGCCCTTTTCATGCTCTCTCTGCGCTTATGCTTTGAGAGC 780
QY 1071 AAGACCCATCTCTGCTTGTGATGAGCTGATGAATGGGGGAGACCTCAAGTTCACATC 1130
Db      |||
781 AAGACCCATCTCTGCTTGTGATGAGCTGATGAATGGGGGAGACCTCAAGTTCACATC 840
QY 1131 TACAACGTGGGACGCGTGGCTTGGACATGAGCGGGGTGATCTTTTACTCGGCCAGATA 1190
Db      |||
841 TACAACGTGGGACGCGTGGCTTGGACATGAGCGGGGTGATCTTTTACTCGGCCAGATA 900
QY 1191 GCCTGTGGGATGCTGCACCTCCATGAACCTCGGCATGCTCTATCGGAGCATGAAGCTGAG 1250
Db      |||
901 GCCTGTGGGATGCTGCACCTCCATGAACCTCGGCATGCTCTATCGGAGCATGAAGCTGAG 960
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QY 1251 AATGTCCTTCTGATGACCTCGGCAACTGACAGTTATCTGACCTGGGGCTGCGCTGGAG 1310
Db |||||
QY 961 AATGTCCTTCTGATGACCTCGGCAACTGACAGTTATCTGACCTGGGGCTGCGCTGGAG 1020
Db |||||
QY 1311 ATGAAGGTGCAAGCCCATCCAGAGGGCTGGACCAATGGTTACATGGCTCTTGAG 1370
Db |||||
QY 1021 ATGAAGGGTGGCAAGCCCATCCAGAGGGCTGGACCAATGGTTACATGGCTCTTGAG 1080
Db |||||
QY 1371 ATCTTAATGAAAGTAAAGTTATTCCTATCTGTGGAGTGGTTGGCCATGGATGGCAGC 1430
Db |||||
QY 1081 ATCTTAATGAAAGTAAAGTTATTCCTATCTGTGGAGTGGTTGGCCATGGATGGCAGC 1140
Db |||||
QY 1431 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAAGAAAAGTTCAGTAAA 1490
Db |||||
QY 1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAAGAAAAGTTCAGTAAA 1200
Db |||||
QY 1491 GAGGATCTGAGCAAGAAAGTCTGCAAGCAGAGTCAAAATTCACAGCATGATTAACCTTACA 1550
Db |||||
QY 1201 GAGGATCTGAGCAAGAAAGTCTGCAAGCAGAGTCAAAATTCACAGCATGATTAACCTTACA 1260
Db |||||
QY 1551 GAGGAAGCAAAAGATATTTGCAAGGCTCTTCTGGCTTAAGAAACCAAGCAAGCTTAGGA 1610
Db |||||
QY 1261 GAGGAAGCAAAAGATATTTGCAAGGCTCTTCTGGCTTAAGAAACCAAGCAAGCTTAGGA 1320
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QY 1611 AGCAGAGAAAAGTCTGATGATCCCAAGGAAACATCATTTCTTTAAACCGATCAACTTTCT 1670
Db |||||
QY 1321 AGCAGAGAAAAGTCTGATGATCCCAAGGAAACATCATTTCTTTAAACCGATCAACTTTCT 1380
Db |||||
QY 1671 CGCTGGAGAGCTGGCTTAATTCGACCCCATTTGTCAGACCCCTTCAGTGGTTTATGCC 1730
Db |||||
QY 1381 CGCTGGAGAGCTGGCTTAATTCGACCCCATTTGTCAGACCCCTTCAGTGGTTTATGCC 1440
Db |||||
QY 1731 AAGACATCGCTGAATGATGATTTCTGAGGTTTCGGGGGTGGAATTTGATGACAAA 1790
Db |||||
QY 1441 AAGACATCGCTGAATGATGATTTCTGAGGTTTCGGGGGTGGAATTTGATGACAAA 1500
Db |||||
QY 1791 GATAAGCAGTTCTTCAAAACATTTTCGACAGGTGCTGTTCTTATAGCATGGCAGGAAGAA 1850
Db |||||
QY 1501 GATAAGCAGTTCTTCAAAACATTTTCGACAGGTGCTGTTCTTATAGCATGGCAGGAAGAA 1560
Db |||||
QY 1851 ATTATAGAAACGGGACTGTTTGAGAACTGAATGATGACCCCAAGACCTTACGGGTTGTAG 1910
Db |||||
QY 1561 ATTATAGAAACGGGACTGTTTGAGAACTGAATGATGACCCCAAGACCTTACGGGTTGTAG 1620
Db |||||
QY 1911 GAGGTAATTCATCAAGTCTGCGGTGTTGTTGTTATTGTAA 1952
Db |||||
QY 1621 GAGGTAATTCATCAAGTCTGCGGTGTTGTTGTTATTGTAA 1662
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RESULT 12

US-10-072-012-273
; Sequence 273, Application US/10072012
; Publication No. US20040033493A1

GENERAL INFORMATION:

; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna

; APPLICANT: Grosse, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 273
; LENGTH: 1701
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-072-012-273

Query Match 74.6%; Score 1640.8; DB 17; Length 1701;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1693; Conservative 0; Mismatches 2; Indels 21; Gaps 3;
QY 273 TGCGCCCGTCTCAGCCATGTTGGACATGGGGGCGCTTGGACCACTGATCGCCCAACACC 332
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QY 333 GCCTACTGTCAGGCGCGGAAGCCCTCGACATGCGACAGCAAGAGCTGCGAGCGGCGGG 392
Db 61 GCCTACTGTCAGGCGCGGAAGCCCTCGACATGCGACAGCAAGAGCTGCGAGCGGCGGG 120
QY 393 CGTAGCCTGGCCCTGCGCGGCTGCGCGAGCTCCGCGCAGAGCTGTCCTCTG 452
Db 121 CGTAGCCTGGCCCTGCGCGGCTGCGAGGCTTGGCGGAGCTCCGCGCAGAGCTGTCCTG 180
QY 453 AACTTCCACAGCCTGTGTGAGCAGCAGCCCATCGGTGCGCGCTTTCGTGACTTCTTA 512
Db 181 AACTTCCACAGCCTGTGTGAGCAGCAGCCCATCGGTGCGCGCTTTCGTGACTTCTTA 240
QY 513 GCCACAGTGCCTCCGTTCCGCAAGCGGCAACCTTCTTAGAGGAGCTGAGAGCTGGAG 572
Db 241 GCCACAGTGCCTCCGTTCCGCAAGCGGCAACCTTCTTAGAGGAGCTGAGAGCTGGAG 300
QY 573 CTGGCCGAGGAGGAGACCCACCAAGACAGCGCTGCGAGGGGCTGCTGGCCACTTGTGG 632
Db 301 CTGGCCGAGGAGGAGACCCACCAAGACAGCGCTGCGAGGGGCTGCTGGCCACTTGTGG 360
QY 633 AGTGCCTCTGCGCGGGGAACCCGCAACCTTCTTAGCCAGCGCGCTGGCCCAAGTGC 692
Db 361 AGTGCCTCTGCGCGGGGAACCCGCAACCTTCTTAGCCAGCGCGCTGGCCCAAGTGC 420
QY 693 CAAGCAGCCACTCTAGGAAAGAGGAGTGGCTGAGCTGCGCGCAAGGCTGAGGCC 752
Db 421 CAAGCAGCCACTCTAGGAAAGAGGAGTGGCTGAGCTGCGCGCAAGGCTGAGGCC 480

QY 753 ATGGCTTTCTTCAAGACGACCCCTTTAAGATTTCTGTGACCAAGCGCTTCTTACGCAAG 812
Db |||||
QY 481 ATGGCTTTCTTCAAGACGACCCCTTTAAGATTTCTGTGACCAAGCGCTTCTTACGCAAG 540
Db |||||
QY 813 TTTCTGAGTGGAAACTCTTTCGAGATGCAACCAAGTGTGACAAAGTACTTCTCACTAGTTTC 872
Db |||||
QY 541 TTTCTGAGTGGAAACTCTTTCGAGATGCAACCAAGTGTGACAAAGTACTTCTCACTAGTTTC 600
Db |||||
QY 873 AGAGTGTCTGGGAAAGGTGGTTTGGGGAGGTATGCGGTGCAAGTGAAGAAACACTGGG 932
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Db |||||
QY 933 AAGATGATGCTGTCTTGAAGAACTGGAACAAGCGGCTGAAGAAAGGTGGCGGAGAAG 992
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QY 646 AAGATGATGCTGTCTTGAAGAACTGGAACAAGCGGCTGAAGAAAGGTGGCGGAGAAG 705
Db |||||
QY 993 ATGGCTCTCTTGAAGAAAGAAATCTTGGAGAGGTGACGAGCCCTTTCATTTGCTCTCTG 1052
Db |||||
QY 706 ATGGCTCTCTTGAAGAAAGAAATCTTGGAGAGGTGACGAGCCCTTTCATTTGCTCTCTG 765
Db |||||
QY 1053 GCCTATGCTCTTGAAGAGAACCCATCTCTGCTTGTGATGAGCTGATGATGGGGA 1112
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QY 766 GCCTATGCTCTTGAAGAGAACCCATCTCTGCTTGTGATGAGCTGATGATGGGGA 825
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QY 1113 GACCTCAAGTTCACATCTCAACAGTGGGCAAGCGTGGCTGACATGAGCCGGGTGATC 1172
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QY 826 GACCTCAAGTTCACATCTCAACAGTGGGCAAGCGTGGCTGACATGAGCCGGGTGATC 885
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QY 1173 TTTTATCTCGGCCAGATAGCTGTGGGATGCTGCACCTCATGAACTCGGATTCGTCTAT 1232
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QY 1066 AATGGTTTACATGCTCCTCAGATCTCTAATGGAAGAGGTAAAGTTATTCCTATCTCTGAC 1125
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QY 1126 TGGTTTGCATGGAGTCAACATTTATGAAATGGTTGCTGGAAGCAACACCATTTCAAAGAT 1185
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QY 1186 TACAAGAAAGGTGAGTAAAGAGATCTGAAAGCAAGAACTCTCTGAAAGACGAGTCAAA 1245
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QY 1530 TTCCAGCATGATAACTTTCAGAGGAAGCAAGATATTTGAGGCTCTTCTTGGCTAAG 1589
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QY 1246 TTCCAGCATGATAACTTTCAGAGGAAGCAAGATATTTGAGGCTCTTCTTGGCTAAG 1305
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QY 1590 AAACAGAGCAACGCTTAGGAAGCAGGAGAGAAAGTCTGATGATCCAGAGAAACATCAT 1646
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QY 1306 AAACAGAGCAACGCTTAGGAAGCAGGAGAGAAAGTCTGATGATCCAGAGAAACATCAT 1365
Db |||||
QY 1647 TTTCTTAAACCATCAACTTTCCTCGCTGAGAGTGGCTTAAATGAAACCCCATTTGTG 1706
Db |||||
QY 1366 TTTCTTAAACCATCAACTTTCCTCGCTGAGAGTGGCTTAAATGAAACCCCATTTGTG 1425
Db |||||
QY 1707 CCAGACCCCTTCAAGTGGTTTATGCCAAAGACATCGCTGAAATTTGATGATTTCTCTGAGTT 1766
Db |||||
QY 1426 CCAGACCCCTTCAAGTGGTTTATGCCAAAGACATCGCTGAAATTTGATGATTTCTCTGAGTT 1485
Db |||||
QY 1767 CGGGGGGTGGAATTTGATGACAAAGATGACGATTTCTTCAAAAACCTTTGCAAGGTGCT 1826
Db |||||
QY 1486 CGGGGGGTGGAATTTGATGACAAAGATGACGATTTCTTCAAAAACCTTTGCAAGGTGCT 1545
Db |||||

QY 1827 GTTCTCTATAGCATGCGAGAGAAATTTATAGAAACGGGACTGTGTTGAGGAATGATGAC 1886
Db |||||
QY 1546 GTTCTCTATAGCATGCGAGAGAAATTTATAGAAACGGGACTGTGTTGAGGAATGATGAC 1605
Db |||||
QY 1887 CCCAACAGACCTTACCGGTTGTGAGAGGGTAAATTCATCAAGTCTGGGCTGTGTTGTTA 1946
Db |||||
QY 1606 CCCAACAGACCTTACCGGTTGTGAGAGGGTAAATTCATCAAGTCTGGGCTGTGTTGTTA 1665
Db |||||
QY 1947 TTGTAATTTGCTCTCTTTTACAGACAGGACGACGGA 1982
Db |||||
QY 1666 TTGTAATTTGCTCTCTTTTACAGACAGGACGACGGA 1701
Db |||||

RESULT 13
US-09-802-117-3
; Sequence 3, Application US/09802117
; Publication No. US20020042503A1
; GENERAL INFORMATION:
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6444561 Human G-Coupled Protein Receptor Kinases and Polynu
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/09/802,117
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/188,449
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-802-117-3

Query Match 47.6%; Score 1046.8; DB 9; Length 1062;
Best Local Similarity 99.8%; Pred. No. 2.6e-305;
Matches 1048; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 291 ATGGTGGACATGGGGGCGCTTGGACAACCTGATGCCAACACCGGCTTACCTGCGAGGCCGG 350
Db 1 ATGGTGGACATGGGGGCGCTTGGACAACCTGATGCCAACACCGGCTTACCTGCGAGGCCGG 60
QY 351 AAGCCCTCGGACTCGGACAGCAAGAGCTGAGCGGGCGGGGCTAGCCTGGCCCTGCC 410
Db 61 AAGCCCTCGGACTCGGACAGCAAGAGCTGAGCGGGCGGGGCTAGCCTGGCCCTGCC 120
QY 411 GGGCTGAGGGCTGCGCGGAGCTCCGCCAGAGCTGTCCCTGAACTTCCACAGCCTGTGT 470
Db 121 GGGCTGAGGGCTGCGCGGAGCTCCGCCAGAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
QY 471 GAGCAGAGCCCATCGGTGCGCGGCTTCCGCTGACTTCTAGGCAAGTGTCCAGCAAGTTC 530
Db 181 GAGCAGAGCCCATCGGTGCGCGGCTTCCGCTGACTTCTAGGCAAGTGTCCAGCAAGTTC 240
QY 531 CGCAAGCGCGCAACCTTCTCTAGAGGAGCTGAGAGCTGCGGAGCTGGCCGAGGAGGACCC 590
Db 241 CGCAAGCGCGCAACCTTCTCTAGAGGAGCTGAGAGCTGCGGAGCTGGCCGAGGAGGACCC 300
QY 591 ACCAAGACAGCGGCTGAGGGGCTGGTGGCCACTTGTGCGAGTGGCCCTGCCCGGGG 650
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QY 651 AACCCGCAACCTTCTCTAGAGGAGCTGAGGAGCTGGCCAGCAAGTGTCCAGCAAGTTC 710
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Db 421 GAAGAGCGAGTGTGCTGAGTGAAGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGAAGAG 480
QY 771 CAGCCCTTTAAGGATTTGCTGACAGGCGCTTCTACAGCAAGTTTCTGCAAGTAACTC 830
Db |||||

; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000638DIV
; CURRENT APPLICATION NUMBER: US/09/964,469
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 60/208,331
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: 09/738,894
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 36651
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(36651)
; OTHER INFORMATION: n = A,T,C or G
US-09-964-469-3

Query Match 39.5%; Score 867.4; DB 9; Length 36651;
Best Local Similarity 95.1%; Pred. No. 3.9e-250;
Matches 895; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
QY 1 GACCTTAAGATGAAGGACCTCACTATAGGCTCGAGCGCGCGCGGCGAGGTCTTC 60
Db 1786 GACCTTAAGATGAAGGACAGTGGGGAGGTGGCGCGGAGGTCTTCACGACGCTTTC 1845
QY 61 GCCTTGGCAGGTGGGAGCATGACCTATCGTGTGCAATTCCTGGCGGGCTATACATAGCCA 120
Db. 1846 GCCTTGGCAGGTGGGAGCATGACCTATCGTGTGCAATTCCTGGCGGGCTATACATAGCCA 1905
QY 121 GTCAAGCTTCTACAAAGAAACCTTTTACACCTCCACGGGTCCACCCACAGGCC 180
Db 1906 GTCAAGCTTCTTACAAGAGAAACCTTTTACACCTCCACGGGTCCACCCACAGGCC 1965
QY 181 ACAGGACTCACTGTAATCCCTTGGACGTTGTCTCACCGGGAAGGAAAGCAGCCAGCA 240
Db 1965 ACAGGACTCACTGTAATCCCTTGGACGTTGTCTCACCGGGAAGGAAAGCAGCCAGCA 2025
QY 241 GCCTCCAGCCCTCTGTGCTTTTCCTGGAGTGGCGCCCGCTGCTCAGCATGTGGACA 300
Db 2026 GCCTCCAGCCCTCTGTGCTTTTCCTGGAGTGGCGCCCGCTGCTCAGCATGTGGACA 2085
QY 301 TGGGGCCCTGGACAACTGATCGCCACACCGCCTACCTGCAGGCCCGGAAGCCCTCGG 360
Db 2086 TGGGGCCCTGGACAACTGATCGCCACACCGCCTACCTGCAGGCCCGGAAGCCCTCGG 2145
QY 361 ACTGGCAGACAAAGAGTGCAGCGCGCGCGGTAGCTGGCCCTGCCCGGCTGCAGG 420
Db 2146 ACTGGCAGACAAAGAGTGCAGCGCGCGCGGTAGCTGGCCCTGCCCGGCTGCAGG 2205
QY 421 GTCGCGGAGTCCCGCAGAAAGTGTCCCTGAACTTCCACAGCTGTGTGAGCAGCAGC 480
Db 2206 GTCGCGGAGTCCCGCAGAAAGTGTCCCTGAACTTCCACAGCTGTGTGAGCAGCAGC 2265
QY 481 CCATCGGTGGCGCCTCTTCGTGACTTCCTAGCCACAGTGCACAGTTCGCCAAGCGG 540
Db 2266 CCATCGGTGGCGCCTCTTCGTGACTTCCTAGCCACAGTGCACAGTTCGCCAAGCGG 2325
QY 541 CAACCTTCTAGAGACGTGCAGAACTGGGAGCTGGCGGAGGAGGCCACCAAGACA 600
Db 2326 CAACCTTCTAGAGACGTGCAGAACTGGGAGCTGGCGGAGGAGGCCACCAAGACA 2385
QY 601 GGGCCCTGAGGGGTGTGTGGCCACTTGTGAGTGTCCCTTGCCTGGGGAAACCGCAAC 660
Db 2386 GGGCCCTGAGGGGTGTGTGGCCACTTGTGAGTGTCCCTTGCCTGGGGAAACCGCAAC 2445
QY 661 CTTCTCTCAGCCAGGCCGTGGCCACCAAGTGCAGCAGCCACCACTGAGGAAGCGAG 720

Search completed: May 11, 2005, 06:54:24
Job time : 2887.42 secs

Db 2446 CTTCTCTCAGCCAGGCCGTGGCCACCAAGTGCACAGCAGCCACCACTGAGGAAGCGAG 2505
QY 721 TGGCTGCAGTGAACGCTGCGCAAGGCTGAGGCATGGCTTTCTTGCAGAGCAGCCCTTTA 780
Db 2506 TGGCTGCAGTGAACGCTGCGCAAGGCTGAGGCATGGCTTTCTTGCAGAGCAGCCCTTTA 2565
QY 781 AGGATTTCTGTGACCAAGCGCTTCTACGACAAAGTTTCTGCAGTGGAAACTCTTCGAGATGC 840
Db 2566 AGGATTTCTGTGACCAAGCGCTTCTACGACAAAGTTTCTGCAGTGGAAACTCTTCGAGATGC 2625
QY 841 AACCAAGTGTCAAGCAAGTACTTCACTGAGTTTCAGAGTCTCGGGGAAAGTGTGTTGGGG 900
Db 2626 AACCAAGTGTCAAGCAAGTACTTCACTGAGTTTCAGAGTCTCGGGGAAAGTGTGTTGGGG 2685
QY 901 AGGTATGTGCGCTCCAGGTGAAACACTGCGGAAGATGTAT 941
Db 2686 AGGTAAAGTGTCTCCAGTAGCCAGGCTAGAAAGTGAAGCAT 2726